Le, Emily

From:

Le, Emily

Sent:

Tuesday, August 03, 2004 9:45 AM

To:

Delaval, Jan

Subject:

RE: sequence search: 09/939537

-----Original Message-----

From:

Delaval, Jan

Sent:

Tuesday, August 03, 2004 5:58 AM

To:

Le, Emily

Subject:

RE: sequence search: 09/939537

I need to know the exact points of fusion for each request, example number 3: 1-394 of # 29 fusion to position 1 of # 32.

-----Original Message-----

From: Le, Emily

Sent: Mond

Monday, August 02, 2004 9:10 AM

To: Delaval, Jan

Subject: sequence search: 09/939537

Hi Jan,

Please provide a search of:

[Le, Emily] 1. Residues 1-395 of SEQ ID NO: 29

- _2_Residues 1-200 of SEQ ID NO: 31__
- 3. Residues 1-394 of SEQ ID NO: 29 fused with SEQ ID NO: 32 [Le, Emily], at position 1 of SEQ ID NO: 32
- 4. Residues 1-200 of SEQ ID NO: 31 fused with SEQ ID NO: 32 [Le, Emily] at position 1 of SEQ ID NO: 32
- 5. Residues 1-395 of SEQ ID NO: 29 fused with SEQ ID NO: 35 [Le, Emily] at position 1 of SEQ ID NO: 35
- 6. Residues 1-200 of SEQ ID NO: 31f used with SEQ ID NO: 35 [Le, Emily] at position 1 of SEQ ID NO: 35
- 7. Residues 1-394 of SEQ ID NO: 29 fused with SEQ ID NO: 32 [Le, Emily] at position 1 of SEQ ID NO: 32, fused with SEQ ID NO: 35 [Le, Emily] at position 1 of SEQ ID NO: 35
- 8. Residues 1-200 of SEQ ID NO: 31 fused with SEQ ID NO: 32 [Le, Emily] at position 1 of SEQ ID NO: 32, fused with SEQ ID NO: 35 [Le, Emily] at position 1 of SEQ ID NO: 35

for the above case. Please provide a printout of the first 100 hits. Thanks, Jan.

Emily Le Mailbox, Remsen 3C18 Office, Remsen, 3C35 (571) 272-0903 (Oldsn) MWW/B 394d SIMI

7,

; Entered [jdelaval 3-Aug-04 11:02]
SEQ1
MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLT
KQPSKLNDRADSRRSLWDQGNFPLIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQQQSLT
LTLESPEGSSEVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLAFQKASSI
VYKKGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPL
HLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAK
VSKREKPVWVLNPEAGWWQCLLSDSGQVLLESNIKVLPTWSTPVH1

; Entered [jdelaval 3-Aug-04 11:05]
SEQ2
MARGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLT
KGPSKLNDRADSRRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSOTHLLQGQSLT
LTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIV1

; Entered [jdelaval 3-Aug-04 11:02] SEQ3

WARGVPFRHLLLVLQLALLPAATOGNKVVLGKKGDTVELTCTASOKKS1OFHWKNSNQIKILGNQGSFLT
KGPSKLNDRADSRRSLMDQGNPPLIIKNLKIEDSDTY1CEVEDOKEEVQLLVFGLTANSDTHLLOGQSLT
LTLESPDGSSPSVQCRSPRGKN1QGGKTLSVSQLELQDSGTMTCTVLQNCKKVEFKIDIVVLAFQKASSI
VYKKEGEQVESSFPLAFTVEKLTGSGELMMQAERASSSKSMITFDLKNKEVSVKRKVDDPKLQNCKKLPL
HLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQKNLTCEVMGPTSPKLMLSLKLENKEAK
VSKREKVMVLNPEAGMWQCLLSDSGQVLLESNIKVLFTWSTPVEPKSCOKTHTCPPCPAPELLGGPSVF
LFPFKFKDTIMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREZQVNSTYRVVSVLTVLHQ
DMLNGKEYKCKVSNKALPAPIEKTISKAKGQPERFPQVTTLPESRDELTKNROVSLTCLUKGFYSDIAVEM
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDE
TCAEAQDGELDGLMTTDP1

; Entered [jdelaval 3-Aug-04 11:05]

SEQ04

MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLT

KGPSKLMDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSFLT

LTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSC

DKTHTCPELLGGPSVFLFPFKPKDTLMISRTPFVTCVVVDVSHEADPEVKFNWYVDGVEVINAKTKPREEQ

YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSL

TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH

YTQKSLSLSPGLQLDETCAEAQDGELDGLWTTDP1

; Entered [jdelaval 3-Aug-04 11:02] SEQ5

MNRGVPFRHLLLVQLALLPAATOGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLT
KGPSKLNDRADSRRSLWDGGNFPLIIKUKIEDSDTYICEVEDDOKEEVQLLVFGLTANSDTHLLQGQSLT
LTLESPPGSSESVQCHSERGKNIQGGKTLSVSQLELQDSGTWTCTVLNQXKXVEFKIDITVLAFQNASSI
VYKKEGEOVEFSFPLAFTVEKLTGSGELWMQAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPL
HLTLPQALPQYAGSGNLTLALBAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSFKLMLSIKLEKKEAK
VSKREKPWVLJUAPEAGWMQCLLSDSGQVLLESNIKVLETWSTPVHPRASALPAPPTGSALPDPQTASALP
DPPAASALPAALAVISFLIGLGVACVLARTR1

; Entered [jdelaval 3-Aug-04 11:05]
SEQ6
MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLT
KGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLT
LTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPRASALPAPP
TGSALPDPQTASALPDPPAASALPAALAVISFLLGLGLGVACVLARTR1

; Entered [jdelaval 3-Aug-04 11:02] SEQ7

MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKS IQFHWKNSNQIKILGNQGSFLT
KGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLT
LTLESPPGSSPSVQCRSPRGKNIQGGKTLSVGQLELQDSGTWTCTVLQNQKKVEEKIDIVVLAFQKASSI
VYKKEGEQVEFSSFPLAFTVEKLTISGELMWQAERASSSKSWITFDLKNKEVSVKRVTQDFKLQNGKKLEL
HLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGFTSPKLMLSLKLENKEAK
VSKREKFVWYLNEEAGMWQCLLSDSGQVLLESNIKVLFTWSTPVCCPAERESQCNCTHTCDETLGGPSVF
LFPFKRDTLMISRTPEVTCVVLVUSHEDPEVKRNWYVDGVEVHNAKTKPREEQXNSTYNVVSVLTVLHQ
DWLNGKEYKCKVSNKALLAPIEKTISKAKGQPREPQVYTLPFSRDELTKAQVSLTCLVKGFYPSDIAVEW
ESNGQEENNYKTTPPVLDSDGSFFLYSKLTVDKGRWQOGNVFSCSVMHEALHNHYTQKSLSLSLSFGLQLDE TCAEAQDGELDGLWTTDP1

; Entered [jdelaval 3-Aug-04 11:05]
SEQ8
MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLT
MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLT
KGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEBVQLLVFGLTANSDTHLLQGQSLT
LTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSC
DKTHTCPELLGGPSVFLFPPKRKDTLMISRTPEVTCVVDVSHEDPEVKFNWTVDGVEVHNAKTKPREQ
YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPEKTISKAKGQPREPQVYTLPPSRDELTKNQVSL
TCLVKGFYPSDIAVEWSSNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGVLPSCSVMEALHNH
YTQKSLSLSPGLQLDETCAEAQDGELDGLWTTDPPRASALPAPPTGSALPDPQTASALPDPPAASALPAA
LAVISFLLGLGLGVACVLARTR1

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Ig gamma-2 chain
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A;Accession: A341...
A;Molecule type: protein
A;Residues: 26-394 <CAR>
R;Lederman, S.; DeMartino, J.A.; Daugherty,
Mol. Immunol. 28, 1171-1181, 1991
A;Title: A single amino acid substitution i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T-cell surface glycoprotein CD4 precursor [validated] - human N;Alternate names: T-cell surface antigen T4/Leu 3 C;Species: Homo sapiens (man) C;Date: 28-May-1996 #sequence revision 31-Dec-1988 #text change 20-Apr-2001 C;Accession: A90872; A32722; A34194; A53287; I54176; I54297; A02109; A30039 R;Maddon, P.J.; Litman, D.R.; Godfrey, M.; Maddon, D.E.; Chess, L.; Axel, R. Cell 42, 93-104, 1955 Cell 42, 93-104, 1955 A;Accession: A90872; MUID:85254948; PMID:2990730 A;Accession: A90872; MUID:85254948; PMID:2990730
A;Molecule type: mRNA
A;Residues: 250-264,'W',266-280
A;Note: sequence extracted from
                                                              A;Reference number: A53287; MUID:92072595; PMID:19
A;Accession: A53287
A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 26-426,428-458
A;Residues: 26-426,628-458
R;Carr, S.A.; Hemling, M.E.; Folena-Wasserman, G.; Sweet,
J. Biol. Chem. 264, 21286-21295, 1989
A;Title: Protein and carbohydrate structural analysis of
A;Reference number: A34194; MUID:90078232; PMID:2592374
A;Contents: disulfide bonds; carbohydrate-binding sites
A;Accession: A34194
                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell 55, 541, 1988
A;Title: Corrected CD4 sequence.
A;Reference number: A90907; MUID:89028665; PMID:3263213
A;Centents: annotation; revision to residue 26
R;Camerini, D.; Seed, B.
Cell 60, 747-754, 1990
A;Title: A CD4 domain important for HIV-mediated syncytium formation lies outside the A;Reference number: A32722; MUID:90182664; PMID:2107024
A;Reference number: A32722
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
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A;Residues: 1-25,'N',27-458 <MAD>
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  from NCBI backbone (NCBIP:68249)
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RESULT RWCZT4 T-cell

surface glycoprotein CD4 - chimpanzee

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C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology C;Keywords: AIDS; duplication; glycoprotein; T-cell; transmembrane protein E;1-25/Domain: signal sequence #status predicted <SIG> F;26-458/Product: T-cell surface glycoprotein CD4 #status experimental <MAT> F;34-111/Domain: immunoglobulin homology <IM1> F;34-111/Domain: immunoglobulin homology *status atypical <IM2> F;316-186/Domain: immunoglobulin homology <IM3> F;216-299/Domain: immunoglobulin homology <IM3> F;321-372/Domain: immunoglobulin homology <IM4> F;397-420/Domain: transmembrane #status predicted <INT> F;41-109,155-184,328-370/Disulfide bonds: #status experimental F;296,325/Binding site: carbohydrate (Asn) (covalent) #status experimental
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Genomics 14, 590-597, 1992

A;Title: A human dimorphism resulting from loss of an Alu.

A;Reference number: I54176; MUID:93052387; PMID:1330888

A;Accession: I54176
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A;Residues: 1-264,'W',266-458 <RE2>
A;Cross-references: GB:M35160; NID:9179143; PIDN:AAA16069.1; PID:9179144
C;Comment: Macrophage tropic strains of HIV-1 bind to a complex of chemokine
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A;Cross-references: GDB:119767; OMIM:186940
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A;Introns: 16/3
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A;Residues: 1-72 <RES>
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Best Local Similarity
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                                                                                                                    LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                                                                               QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
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                                           LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVEP
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LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVQP
                                                                                            LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKAVWV
                                                                                                                                                                                         QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
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Pred. No. 1.7e-112;
1; Mismatches 2;
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RESULT 3
RMMQT4
T-cell surface glycoprotein CD4 -
N;Alternate names: T-cell surface
C;Species: Macaca mulatta (rhesus
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C;Comment: This protein is expressed on most thymocytes, on a subset of mature of C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology c;Keywords: duplication; glycoprotein; T-cell; transmembrane protein F;1-432/Product: T-cell surface glycoprotein CD4 #status predicted <MAT>
F;1-371/Domain: immunoglobulin homology <IM1>
F;9-86/Domain: immunoglobulin homology <IM1>
F;111-161/Domain: immunoglobulin homology <IM3>
F;191-274/Domain: immunoglobulin homology <IM3>
F;191-274/Domain: immunoglobulin homology <IM3>
F;372-395/Domain: intransmembrane #status predicted <TMM>
F;372-395/Domain: intransmembrane #status predicted <IM7>
F;36-84,130-159,303-345/Disulfide bonds: #status predicted <IM7>
F;271,300/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Species: Pan troglodytes (
C;Date: 30-Sep-193 #sequenc
C;Accession: B32722; A46534
R;Camerini, D.; Seed, B.
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A;Cross-references: GB:M31135
A;Cross-references: GB:M31135
R;Fomegaard, A.; Hirsch, V.M.; Johnson, P.R.
Eur. J. Immunol. 22, 2973-2981, 1992
Eyr. J. Immunol. 22, 2973-2981, 1992
A;Title: Cloning and sequences of primate CD4 molecules: A;Reference number: A46534; MUID:93049640; PMID:1425921
A;Recession: A46534
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;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
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Matches 364; Conserv
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macaque)
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                                                rhesus macaque
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C;Comment: This protein is expressed on most thymocytes, on a subset of C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology C;Keywords: duplication; glycoprotein; T-cell; transmembrane protein F;1-432/product: T-cell surface glycoprotein CD4 #status predicted <MAT> F;1-371/Domain: extracellular #status predicted <EXT> F;9-86/Domain: immunoglobulin homology <IM1> F;111-161/Domain: immunoglobulin homology #status atypical <IM2> F;80-293/Domain: immunoglobulin homology <IM3> F;296-347/Domain: immunoglobulin homology <IM4> F;372-395/Domain: intransmembrane #status predicted <IMM'> F;372-395/Domain: intracellular #status predicted <IMM'> F;36-84,130-159,303-345/Disulfide bonds: #status predicted <IMS F;16-84,130-159,303-345/Disulfide <IMS F;16-84,130-159,303-345/Disul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-432 < CAM>
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A;Title: A CD4 domain important for HIV-mediated syncytium A;Reference number: A32722; MUID:90182664; PMID:2107024
A;Accession: C32722
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Best Local S
Matches 335
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                                                           LPTWSTPVEP 396
                                                                                                                                                       TCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNIKV
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VPTWPTPVQP 371
                                                                                                                                                                                                                                                                                   TQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQKNL
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                                                                                                                      TCEVWGPTSPKLTLSLKLENKGATVSKQAKAVWVLNPBAGMWQCLLSDSGQVLLESNIKV
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Pred. No. 1.3e
17; Mismatches
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C;Species: Homo sapiens (man)
C;Date: 31-Jan-1901 #sequence revision 18-Aug-1982 #text change 16-Jul-1999
C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A;Title: The nucleotide sequence of a human immunoglobulin C-gammal gene.
A;Reference number: A93433; MUID:82274238; PMID:6287432
A;Accession: A93433

GHA

Ig gamma-1 chain C region -

human

A;Cross-references: EMBL:Z17370
A;Note: this sequence has the G1m(17) alloty;
A;Note: Lys-330 is removed after translation

allotypic

marker,

97-Lys,

and

the G1m(1)

markers

A; Molecule type: DNA A; Residues: 1-330 <ELL>

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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 88-113;235-330 <TAK>
A; Crose-references: EMBL: 217370
A; Crunningham, B.A.; Rutishauser, U.; Gall, W.F.
Biochemistry 9, 3161-3170, 1970
A; Title: The covalent structure of a human gall A; Reference number: A90563; MUID: 71064024; PM
                                                                                                                                                                                                                                                                  A;Note: this sequence has the Gim(3) and Gim(non-1) markers R;Gall, W.S.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobul A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of enbromide cleavage products and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E',
A; Note: this sequence has the Gim(17) and Gim(1) markers
R; Schmidt, W.E; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A; Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgGl |
A; Reference number: A91723; MUID:83289131; PMID:6884994
A; Contents: myeloma protein KOL; disulfide bonds
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IQA and IGM, the subunits associate int C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; 91ycoprotein; heterotetramer; immunoglobulin F;20-85/Domain: immunoglobulin homology <IM1>
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A;Title: The covalent structure of a human A;Reference number: A90564; MUID:71064025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Takahashi, N.; Ueda, S.; Obata, M.; Nikai Cell 29, 671-679, 1982
A;Title: Structure of human immunoglobulin A;Reference number: $33887; MUID:83001943; A;Accession: $33887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data A;Reference number: S33904 A;Accession: S36861
                                                                                                                                                            A; Cross-references: GDB:120085; Ol
A; Map position: 14q32.33-14q32.33
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R;Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357,
A;Title: Die Primaerstruktur eines moi
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                                                                                                                                                                                                                     A;Gene: GDB:IGHG1
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A;Accession: B91668
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A;Residues: 136-154,'Q',1
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A;Residues: 1-96,'R',98-135 <CUN>
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,,Rosidues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330
...Note: this sequence has the Glm(3) and Glm(non-1) markers
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as the Glm(non-1) markers, 239-Glu and 241-Met
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Bennett,
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pMID:4923144
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pMID:5530842
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pMID:5489771
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PMID:6811139
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, C.; Konigsberg, W.H.; Edelman,
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Ig gamma-1 chain C region - synthetic
C;Species: synthetic
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: 331866
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S31866
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F;243-310/Domain: immunoglobulin homology <IM3>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status
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A; Residues: 1-255 <FIL>
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                                                                                                                                                             FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 513
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                         PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHBALHNHYTQKSLSLSPG
                                                                                       TISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
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                                                                   TISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTT
                                                                                                                                       FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 142
                                                                                                                                                                                                            VESKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 82
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Pred. No. 8e-68;
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protein-protein
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A; Molecule type: mRNA

A; Residues: 1-234 <EHR>

A; Residues: 1-234 vehre*

C; Superfamily: immunoglobulin C region; immunoglobulin homology

C; Keywords: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                             Ig gamma chain C region - chimpanzee (Species: Pan troglodytes (chimpanzee) C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999 C;Accession: PT0207 R;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L. Mol. Immunol. 28, 319-322, 1991 A;Title: Nucleotide sequence of chimpanzee Fc and hinge regions. A;Reference number: PT0207; MUID:91287716; PMID:2062315 A;Accession: PT0207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: $6:339; $7:2664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Bur. J. Biochem. 229; $4-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: $6:9339; MUID:95262687; PMID:7744049
A;Accession: $6:9339
                                                                                В
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A; Residues: 1-140, 'C', 142-374 <KH2>
A; Cross-references: EMBL: X81695
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R;Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: S72664
A;Accession: S72664
A;Accession: S72664
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A; Residues: 1-374 < KHA>
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                                                                                                                                                                   Query Match 35.7
Best Local Similarity 95.4
Matches 227; Conservative
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Best Local Similarity
Matches 229; Conserv
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Species: Homo sapiens (man)
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                                                                                SNIKVLPTWSTPVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
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                        VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 501
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VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK
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95.4%;
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99.1%;
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7:
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                                                                                                                                                                 Score 1218; DB 2;
Pred. No. 3.6e-65;
1; Mismatches 6
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Pred. No. 5.9e-67;
2; Mismatches 0;
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R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, A;Reference number: A60764; MUID:90007613; PMID:2571587
A;Accession: A60764
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
C;Superfamily: immunoglobulin C region; immunoglobulin PC;Keywords: immunoglobulin
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A;Gene: GDB:IGHG3
A;Gross-references: GDB:I19339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                               Ig gamma-3 chain C region, form LAT - human
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C;Accession: A60764
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A;Tille: Sequence of a human immunoglobulin gamma 3 heavy cha A;Reference number: A23511; MUID:86148507; PMID:3081877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig gamma-3 chain C region (allotype G3m(b)) - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change C;Accession: A23511
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A; Residues: 1-377 < HUC>
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                                          immunoglobulin homology <IMM>
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    34.2%;
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  Score 1169;
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Pred. No. 4e
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Ig gamma-3 heavy chain disease proteins - human

(;Species: Homo sapiens (man)

C;Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999

C;Accession: A90442; A92219; A90198; A93915; A02149

R;Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.

Biochemistry 19, 4304-4308, 1980

A;Title: Primary structure of human gamma3 immunoglobulin deletion mutant: QA;Reference number: A90442; MUID:81021548; PMID:6774747

A;Contents: heavy chain disease protein Wis
A;Cross-references: GDB:119339;
A;Map position: 14q32.33-14q32.
C;Superfamily: immunoglobulin C
                                                                                                                                                A; Note: a carboxyl-terminal Lys is removed posttranslationally A; Note: this sequence may represent an allelic form or another C; Comment: The heavy chain disease protein Wis is shown.
                                                                                                                                                                                                                                                                                                             A;Title: gamma heavy chain disease in man: cDNA sequence A;Reference number: A93915; MUID:82247835; PMID:6808505 A;Contentes heavy chain disease protein Omm A;Accession: A93915
                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Molecule type: protein
A; Residues: 59-125, 'BB', 128-226, 228-289 < WOL>
A; Residues: 59-125, 'BB', 128-226, 228-289 < WOL>
A; Note: this protein lacks most of the V region, all of the CH1 region, and part of R; Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, Proc. Natl. Acad. Sci. U.S.A. 79, 3360-3364, 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 7 R;Wollenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C. Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A;Title: The amino acid sequence of "heavy chain disease" protein ZUC. Struc A;Reference number: A90198; MUID:77021516; PMID:823945
A;Contents: heavy chain disease protein Zuc, partial sequence corresponding A;Cocession: A90198
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A;Residues: 12-97 <MIC>
A;Note: the hinge region in gamma-3 chains is about four times as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchair A;Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 cd A;Note: the sequence of residues 42-76 was taken from the reference that follows R;Michaelsen, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
A;Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication A;Reference number: A92219; MUID:77118561; PMID:402363
A;Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein WA;Accession: A92219
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                                                                                             A;Gene: GDB:IGHG3
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A;Residues: 12-70;72-114;116-125,'E',127-133,'L',135-136,'E',138,'Y',140-154,'D'
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A;Residues: 1-289 <FRA>
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8; Mismatches 9;
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Best Local Similarity
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                                                                                                              ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 574
                                          PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                  ISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTP
                                                                                                                                                                              KWYVDGVQVHNAKTKPREQQFNSTFRVVSVLTVLHQNWLDGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                     EPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF 118
                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                  33.7%;
                                                                                                                                                                                                                                                                                                                                                          Score 1151; DB 1;
Pred. No. 4.3e-61;
3; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                              178
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A;Residues: 1-326 <ELL>
A;Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1;
A;Note: Lys-326 is probably removed posttranslationally
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A;Molecule type: protein
A;Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <W
A;Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <W
A;Note: Trp-156 is at or near the complement-binding site
R;Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A;Title: The amino acid sequences of the three heavy chain
A;Reference number: A90752; MUID:80001357; PMID:113060
                                                                                                                                                                                                                                                                                       A; Title: The primary structure of a human IgG2 heavy chain: A; Reference number: A92809; MUID:81007873; PMID:6774012 A; Contents: myeloma protein Til
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-326 <E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change C;Date: 30-Apr-1980; A92809; A90752; A93132; A02148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin
A;Reference number: A93906; MUID:82197621; PMID:6804948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Ellison, J.; Hood,
                                                                                                                                                                                                                                                             A; Accession: A92809
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                                                                                                                                                                                                                                                                                                                                                                  genetic,
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                                                                                                                                                                                                                                                                                                                                                                      evolutionary,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PID:g6066056
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A;Molecule type: protein
A;Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-;
A;Note: this sequence has since been revised

R;Hofmann, T.; Parr, D.M. Mol. Immunol. 16, 923-925, 1979

A;Contents: myeloma protein A;Accession: A90752

Zie

constant region domains

ō, ø and

A;Title: A note on the amino acid sequence of residues 381-391 A;Reference number: A93132; MUID:80114419; PMID:118920

ō,

human immunoglobulin

A; Molecule type: protein A; Residues: 238-275 < HOF>

A;Accession: A93132 A; Contents: Zie

submitted to the Atlas, March

1980

number: A94591 annotation; Zie,

revisions to residues 25, differs from that shown i

in having

59, 60,

and 264-268 60-Ala and

ij

the

T.; Parr, D.M.

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RyMilstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin (A;Title: Disulphide bridges of the heavy chain of human immunoglobulin (A;Contents: annotation; myeloma protein Sa, disulfide bonds R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID:6964124; PMID:5782707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GDB:119338; OMIM:147110

A;Cross-references: GDB:119338; OMIM:147110

A;Cross-references: GDB:119338; OMIM:147110

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap complex: An immunoglobulin beterotetramer subunit consists of two identical light (kap cycle family: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;20-85;Domain: immunoglobulin homology <IM1>
F;133-202/Domain: immunoglobulin homology <IM2>
F;133-202/Domain: immunoglobulin homology <IM2>
F;139-306/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental F;27-83,140-200,246-304/Disulfide bonds: #status experimental F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
                                                                                                                                                                                                                                  C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: A46254
R;Hague, B.F.; Sawasdikosol, S.; Brown, T.J.; Lee, K.; Recker, D.P.; Kindt, Proc. Natl. Acad. Sci. U.S.A. 89, 7963-7967, 1992
A;Title: CD4 and its role in infection of rabbit cell lines by human immuno. A;Reference number: A46254; MUID:92390370; PMID:1518821
A;Accession: A46254
A;Status: preliminary
A;Status: preliminary
                                                                            A; Molecule type: mRNA
A; Residues: 1-459 < HAG>
A; Residues: GB:M92840; NID:g164871; PIDN:AAA31198.1; PID:g164872
A; Mote: sequence extracted from NCBI backbone (NCBIN:112732, NCBIP:112733)
A; Note: sequence extracted from NCBI backbone (NCBIN:112732, NCBIP:112733)
C; Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology
C; Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology
C; Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology
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A46254
CD4 precursor -
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  Query Match
Best Local Sin
Matches 243;
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Best Local Similarity
Matches 217; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNIKVLPTWSTPVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
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                         33.7%;
  66;
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Score 1149; DB
Pred. No. 1e-60;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1150; DB 1;
Pred. No. 5.8e-61;
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                                      2;
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                                             Length 459;
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  20;
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A;Note: the sequence was determined from the R;Pink, J.R.L.; Buttery, S.H.; De Vries, G. Biochem. J. 117, 33-47, 1970
A;Title: Human immunoglobulin sublclasses.
A;Reference number: A90249; MUID:70207560;
A;Accession: A90249
                                                                                                                                                          hain disulfide bonds. In some cases, such as IgA and IgM, the subunity (5/Superfamily: immunoglobulin C region; immunoglobulin homology C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;20-85/Domain: immunoglobulin homology <IM1>
F;99-110/Region: hinge
F;134-203/Domain: immunoglobulin homology <IM2>
F;240-307/Domain: immunoglobulin homology <IM3>
F;240-307/Domain: immunoglobulin homology <IM3>
F;147/Disulfide bonds: interchain (to light chain) #status experimental F;27-83,141-201,247-305/Disulfide bonds: #status predicted F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                      A;Cross-references: GDB:119340; OMIM:147130
A;Map position: 14432.33-14432.33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap)
                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein A;Residues: 1-30;81-326 C;Genetics: A;Gene: GDB:IGHG4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 A;Reference number: A90933; MUID:83157104; PMID:6299662 A;Accession: A90933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-327 <ELL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision
C;Accession: A90933; A90249; A02150
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RESULT 14

$30193

T-cell surface glycoprotein CD4 - dog
C; Species: Canis lupus familiaris (dog)
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change  
C; Accession: $30193
R; Milde, K,F.; Conner, G.E.; Mintz, D.H.; Alejandro, R.
Biochim. Biophys. Acta 1172, 315-318, 1993
A; Title: Primary structure of the canine CD4 antigen.
A; Reference number: $30193; MUID:93192324; PMID:7916632
A; Accession: $30193
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A;Molecule type: mRNA
A;Residuse: 1-432 <MIL>
A;Residuse: 1-432 <MIL>
A;Cross-references: EMBL:X68565; NID:g288652; PIDN:CAB37664.1;
C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin :
C;Keywords: glycoprotein C
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                                                                                                                                                                               QGASSSLLWISFTLENRKLSMKEAHAPLKLOMKESLPLRFTLPOVLSRYAGSGILTLNL-
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                                                                                                  AKTGKLHQEVNIVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLN
                                                                                                                                                                                                                                   ERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALE 302
                                                                                                                                                                                                                                                                                                 TCIISQSQXTVEFNINVLVLAFQXVSNTFYAREGDQVEFSFPLSFEDENLV--GELRWQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----NSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTW 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSSRLKHRVESKKNLWDQGSFPLVIKDLEVADSGIYFCDT-DKRQEVELLVFNLTAKWDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LMLQLVMLPAVTPVREVVLGKAGDAVELPCQTSQKKNIHFNWRDSSMVQILGNQGSFWTV 60
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                                                             AK-GTLYQEVNLVVMRANSSQNNLTCEVLGPTSPELTLSLNLKEQAAKVSKQQKLVWVVD
                                                                                                                                                                                                                                                                                                                                                        TCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQA
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Pred. No. 2e-60;
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Pred. No. 3.8e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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A; Contents: annotation
C; Superfamily: T-cell surface glycoprotein CD4; immunoglobulin
C; Keywords: glycoprotein; membrane protein; surface antigen
C; Keywords:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M15768; NID:g203387; PIDN:AAA40901.1; PID:g203388 R;Davis, S.J.; Ward, H.A.; Puklavec, M.J.; Willis, A.C.; Williams, A.F.; J. Biol. Chem. 265, 10410-10418, 1990 A;Title: High level expression in Chinese hamster ovary cells of soluble A;Reference number: A35433; MUID:90285164; PMID:2113054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 21-Jan C;Accession: A27449; A35433 R;Clark, S.J.; Jefferies, W.A.; Barclay, A.N.; Gagnon, J.; Williams, A Proc. Natl. Acad. Sci. U.S.A. 84, 1649-1653, 1987 A;Title: Peptide and nucleotide sequences of rat CD4 (W3/25) antigen: A;Reference number: A27449; MUID:87175535; PMID:3104900 A;Accession: A27449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T-cell surface glycoprotein CD4 precursor N;Alternate names: W3/25 antigen C;Species: Rattus normania...
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A; Residues: 1-457 < CLA>
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                                                                                                                                                                       IKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEV
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                                  PVWVLNPEAGMWQCLLSDSGQVLLESNIKVL
                                                                        TLTLD--RGILYQEVNLVVMKVTQPDSNTLTCEVMGPTSPKMRLILKQENQEARVSRQEK
                                                                                                             TLALEAKTGKLHQEVNLVVMRATQLQKN-LTCEVWGPTSPKLMLSLKLENKEAKVSKREK
                                                                                                                                                     LRWKAEKAPSSQSWITFSLKNQKVSVQKSTSNPKFQLSETLPLTLQIPQVSLQFAGSGNL
                                                                                                                                                                                                                                  DSGIWNCTVTLNQKKHSFDMKLSVLGFASTSITAYKSEGESAEFSFPLNLGEESL--QGE
                                                                                                                                                                                                                                                                    DSGTWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGE
                                                                                                                                                                                                                                                                                                             ELWVFRVTFNPGTRLLQGQSLTLTLDSNPKVSDPPIECKHKSSNIVKDSKAFSTHSLRIQ
                                                                                                                                                                                                                                                                                                                                               QLLVFGLTANSDTHLLQGQSLTLTLES-PPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQ
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Pred. No. 7.7e-52;
1; Mismatches 115
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C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999
C;Accession: A02110; A26038; A39893; A39955; I54564; I69018; A47642
C;Accession: A02110; A26038; A39893; A39955; I54564; I69018; A47642
R;Tourvieille, B.; Gorman, S.D.; Field, E.H.; Hunkapiller, T.; Parnes, J.R. Science 234, 610-614, 1986
Science 234, 610-614, 1986
A;Title: Isolation and sequence of L3T4 complementary DNA clones: expression A;Reference number: A02110; MUID:87018845; PMID:3094146 T-cell surface glycoprotein CD4 precursor - mouse N, Alternate names: T-cell differentiation antigen L3T4; T-cell surface antigen ä T4/Leu н cells

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A;Introne: 18/1; 74/1; 128/1; 207/1; 319/1; 386/1; 425/3; 448/2
C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology
C;Keywords: alternative initiators; duplication; glycoprotein; T-cell; transm
F;1-26/Domain: signal sequence #status predicted <SIG-
F;27-457/Product: T-cell surface glycoprotein CD4 #status experimental <MAT>
F;35-114/Domain: immunoglobulin homology <*IN1>
F;35-114/Domain: immunoglobulin homology #status atypical <IM2>
F;20-301/Domain: immunoglobulin homology <IM3>
F;21-372/Domain: immunoglobulin homology <IM3>
F;21-372/Domain: immunoglobulin homology <IN4>
F;35-114/Domain: immunoglobulin homology <IN4>
F;35-119/Domain: immunoglobulin homology <IN4>
F;31-372/Domain: immunoglobulin homology <IN4>
F;321-372/Domain: immunoglobulin homology <IN4>
F;321-372/Domain: immunoglobulin homology <IN4-
F;395-419/Domain: transmembrane #status predicted <INT>
F;420-457/Domain: intracellular #status predicted <INT>
F;420-12;159-188,328-370/Disulfide bonds: #status predicted <INT>
F;420-12;159-188,328-370/Disulfide bonds: #status predicted <INT>
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A; Residues: 1-25, E', 27-457 <GOR>
A; Residues: 1-25, E', 27-457 <GOR>
A; Cross-references: GB:M17080; GB:J03003; NID:g192515; PIDN:AAA37402.1; PID:g387124
R; Maddon, P.J.; Molineaux, S.M.; Maddon, D.E.; Zimmerman, K.A.; Godfrey, M.; Alt, F.W.;
Proc. Natl. Acad. Sci. U.S.A. 84, 9155-9159, 1987
A; Title: Structure and expression of the human and mouse T4 genes.
A; Reference number: A39955; MUID:88097446; PMID:3501122
A; Accession: A39955
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A;Accession: A47642
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A; Residues: 208-318 «RE2»
A; Cross-references: GB:M36851; NID:g198672;
R; Classon, B.J.; Tsagaratos, J.; Kirszbaum,
Immunogenetics 23, 129-132, 1986
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A;Residues: 25-457 <MAD>
A;Note: the Cited GenBank accession number, J03564, is not R;Parnes, J.R.; Hunkapiller, T.
Immunol. Rev. 100, 109-127, 1987
A;Title: L374 and the immunoglobulin gene superfamily: New A;Reference number: I54564, MUID:88152875; PMID:3326818
A;Accession: I54564
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A;Residues: 1-457 <RES>
A;Cross-references: GB:M36850; NID:g198670;
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A; Residues: 1-457 < LIT>
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Matches 211
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;Cross-references: GB:M13816; NID:g192070; PIDN:AAA37267.1; PID:g309112
·1.1rtman. D.R.; Gettner, S.N.
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                                                                                                                                                                                                                                                                                                   298,323,392/Binding site: carbohydrate
                                                                                                                                                                                          Similarity
                                                                     MNRGVPFRH-LLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQI
       MCRAISLARLLLLLQLSQLLAVTQGKTLVLGKEGESAELPCESSQKKITVFTWKFSDQR
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                                                                                                                                                       Conservative
                                                                                                                                                   29.1%; Score 993; DB 1; 53.8%; Pred. No. 1.7e-51; tive 62; Mismatches 109
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L.; Maddox, J.; Mackay, C.R.
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A;Residues: 1-398 <WEL>
A;Residues: 1-398 <WEL>
A;Cross-references: GB;J00451; NID;g194392; PIDN:AAB59655.1; PID:g194433
A;Cross-references was determined from the germline gene
R;Komaromy, M.; Clayton, L.; Rogers, J.; Robertson, S.; Kettman, J.; Wal
Nucleic Acids Res. 11, 6775-6785, 1983
A;Title: The structure of the mouse immunoglobulin in gamma-3 membrane g
A;Reference number: A02155; MUID:84041483; PMID:6314258
A;Accession: A02155
                                                                                                                                                                                                                                                                                                                                 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobu C;KeyBondin: immunoglobulin homology <IM1>
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A; Residues: 328-332,'G',334-341,'Q',343-387,'F',389-398 < XOM>
A; Cross-references: GB: K00698
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R;Wels, J.A.; Word, C.J.; Rimm, D.; Der-Balan, G.P.; Martinez, H.M.; Tucker, EMBO J. 3, 2041-2046, 1984
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  64
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                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KPVWVLNPEAGMWQCLLSDSGQVLLESNIKVL 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GELWWQAERASSSKSWITFDLKNKEVSVKRVTQDFKLQMGKKLPLHLTLPQALPQYAGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VQDSDFWNCTVTLDQKKNWFGMTLSVLGFQSTAITAYKSEGESAEFSFPLNFAEE--NGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LODSGTWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGS
SSLVTVPSSTWPSQTVICNVAHPASKTELIKRIEPRIPKPSTPPGSSCPPGNILGGPSVF
                                               SNIKVLPTWSTPVEPKSCDKTH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVVQVVAPETGLWQCLLSEGDKVKMDSRIQVL 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NLTLTLD--KGTLHQEVNLVVMKVAQLNNTLTCEVMGPTSPKMRLTLKQENQEARVSEEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NLTLALEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GELMWKAEKDSFFQPWISFSIKNKEVSVQKSTKDLKLQLKETLPLTLKIPQVSLQFAGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVELWVFKVTFSPGTSLLQGQSLTLTLDSNSKVSNPLTECKHKKGKVVSGSKVLSMSNLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVQLLVFGLTANSDTHLLQGQSLTLTLES-PPGSSPSVQCRSPRGKNIQGGKTLSVSQLE 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KILGNQG-SFLTKG--PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKE
                                                                                                                                                                                       immunoglobulin homology <IM2>
immunoglobulin homology <IM3>
transmembrane #status predicted <TMM>
intracellular #status predicted <INT>
site: carbohydrate (Asn) (covalent) #
                                                                                                                   27.8%;
                                                                                            44;
                                                                                                                   Score 947.5; DB 1;
Pred. No. 7.2e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from the germline
                                                                                               Mismatches
                                               TCPP---CPAPELLGGPSVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                            #status
                                                                                               Indels
                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kettman, J.; Wall,
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                                                                                                                                            398;
                                                                                                                                                                                            predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         membrane gene segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                            21;
                                                                                          Gaps
  123
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421 LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR 480

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C;Acce88ion: 80/137; Acce., C., Ridioka, T.; Nawanami, --, R;Honjo, T.; Obata, M.; Yamawaki-Kataoka, Y.; Kataoka, T.; Nawanami, --, Cell 18, 559-568, 1979
Cell 18, 559-568, 1979
A;Title: Cloning and complete nucleotide sequence of mouse immunoglobulin gammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 18
GlMSM
GlMSM
GlMSM
Ig gamma-1 chain C region, membrane-bound form - mouse
Ig gamma-1 chain C region, membrane-bound form - mouse
C;Species: Mus musculus (house mouse)
C;Species: 17-Dec-1982 #sequence revision 31-Mar-1991 #text_change 16-Jul-1999
C;Date: 17-Dec-1982 #sequence revision 31-Mar-1999
C;Date: 17-Dec-1982 #sequence revision 31-Mar-1999
C;Date: 17-Dec-1982 #sequence revision 31-Mar-1999
C;Date: 17-Dec-1982 #sequence revision 31-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Introns: 1/1; 98/1; 111/1; 218/1; 323/1; 366/3
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobu
                                       δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:J00453
A;Note: the sequence was determined from the germline gene
R;Tyler, B.M.; Cowman, A.F.; Gerondakis, S.D.; Adams, J.M.; Bernard, O.
Proc. Natl Acad. Sci. U.S.A. 79, 2008-2012, 1982
A;Title: mRNA for surface immunoglobulin gamma chains encodes a highly conserved A;Reference number: A02160; MUID:82197626; PMID:6804950
A;Accession: A02160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ঠ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 323-366 <ROG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell 26, 19-27, 1981
A;Title: Gene segments encoding transmembrane carboxyl termini of immunoglobulin A;Reference number: A02158; MUID:82115295; PMID:6799207
A;Accession: B02158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 323-393 <TYL>
R;Rogers, J.; Choi, E.; Souza, L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;131-200/Domain:
;340-357/Domain:
;358-393/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;340-357/Domain: transmembrane #status predicted <TMM>
;358-393/Domain: intracellular #status predicted <INT>
;174,278/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Keywords: alternative splicing; duplication; c; 131-200/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Residues: 1-393 <HON>
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local (
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                                                                                                                                                                                                                                                   87
                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                    SKDDPEVQPSWFVDDVEVHTAQTQPREEQPNSTFRSVSELPIMHQDWLNGKEFKCRVNSA
                                                                                                                                                                                                                                                                                                               PTWSTPVEPKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 445
                                   ALPAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGO
                                                                                                                                                                           SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGELDGLWTT 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN 540
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   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       27.5%;
                                                                                                                                                                                                                                                                                                                                                                                46;
Score 940.5; DB 1
Pred. No. 1.8e-48;
16; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carter,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    c.;
   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Word,
                                                                                                                                                                                                                                                                                                                                                                                       45;
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                                       565
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                                                                                                           203
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A;Molecule type: protein
A;Molecule type: protein
A;Residues: 129-131;155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'Q',;
A;Rote: this has the e15 allotypic marker, 185-Ala
C;Complex: An immunoglobulin heteroretramer subunit consists of two identical light (kap;
hain disulfide bonds. In some cases, such as IQA and IGM, the subunits associate into lar
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heteroretramer; immunoglobulin
F;20-82/Domain: immunoglobulin homology <IMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 132-143,'E',145-161 <FRU>
A;Residues: 132-143,'E',145-161 <FRU>
R;Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127,
A;Reference number: A94416
A;Accession: A94416
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A;Residues: 88-103,'M',105-143,'E',145-184,'A',186,'E',188-266 <MAR>
A;Residues: 88-103,'M',105-143,'E',145-184,'A',186,'E',188-266 <MAR>
A;Cross-references: GB:M16426; NID:g165111; PIDN:AAA31289.1; PID:g165112
A;Note: this sequence has the dil allotypic marker, 104-Met, and the el5
R;Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
Blochem. J. 116, 249-259, 1970
A;Title: Sequence studies of the Fd section of the heavy chain of rabbit
A;Reference number: A90245; MUID:70110015; PMID:5461106
A;Accession: A90245
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A; Residues: 1-323 <BER>
A; Note: this sequence has
R; Pratt, D.M.; Mole, L.E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L. Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
A;Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding A;Reference number: A93928; MUID:83299917; PMID:6193512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. J. 151, 337-349, 1975
A;Title: Sequence studies on the constant I
A;Reference number: A90290; MUID:76135469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Nucleotide sequence of a rabbit IgG heavy chain A;Reference number: A91749; MUID:84030930; PMID:6313520 A;Accession: A91749
                                                                                                                                                                                                                                                                                                                                         F;130-199/Domain: immunoglobulin homology <IM2>F;236-303/Domain: immunoglobulin homology <IM3>
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A; Residues: 1-47, 'E', 49-71, 'PV', 72-128 < PRA>
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169; Conserv
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                                                                                                                                                                                     Score 922; DB 1; 1
Pred. No. 1.8e-47;
0; Mismatches 37;
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A;Introns: 1/1; 98/1; 114/1; 224/1; 329/1; 372/1
G;Complex: An immunoglobulin heteroterramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate int C;Superfamily: immunoglobulin C region; immunoglobulin homology G;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunog f;137-206/Domain: immunoglobulin homology <IMM>
F;136-303/Domain: transemenbrane #status predicted <IMM>
F;364-399/Domain: intracellular #status predicted <IMM>
F;164-399/Domain: intracellular #status predicted <IMM>
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R;Hall, B.; Milcarek, C.
Mol. Immunol. 26, 819-826, 1989
A;Title: Sequence and polyadenylation site determination of the murine immunoglobulin A;Reference number: 157809; MUID:90097953; PMID:2513486
A;Accession: 157809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 373-399 ARES>
A;Residues: 373-399 ARES>
A;Cross-references: GB:M35032; NID:g194478; PIDN:AAA37919.1; PID:g387217
C;Comment: The sequence of residues 1-328 was assumed to be identical with the correspon C;Comment: Cell lines producing IgG contain two mRNA species for Ig gamma chains. The matin the contains an alternative 3' end, encoded in separate exons, that is homologous with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:J00471
A;Note: the sequence was determined from the germline gene
R;Yamawaki-Kataoka, Y.; Miyata, T.; Honjo, T.
Nucleic Acids Res. 9, 1365-1381, 1991
A;Title: The complete nucleocide sequence of mouse immunoglobulin gamma 2 A gene and A;Reference number: A32657; MUID:81198976; PMID:6262729
A;Accession: B32657.
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A; Residues: 329-399 < YAM>
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Ig gamma 2a chain constant region - pig (fragment) C;Species: Sus scrofa domestica (domestic pig) C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000 C;Accession: I47159 R;Kacskovics, I.; Sun, J.; Butler, J.E.
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R; Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A; Title: Five putative subclasses of swine
A; Reference number: I47158; MUID:95015845;
A; Accession: I47160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig gamma 2b chain constant region - pig (fragment) C;Species: Sus scrofa domestica (domestic pig) C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: immunoglobulin C region; immunoglobulin homology F;133-202/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: IgG2b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; translated
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R; Kacskovics, I.; St
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 26.7%; Score 911.5; DB 2; Local Similarity 63.1%; Pred. No. 7.6e-47;
  294
                                        592
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                                                                                                                                                                                                         474
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                                                                                                                                                                                                                                              SPGPSVFIFPEXPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEE
                       DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                             ABELSRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGTYFLYSKFSV
                                                                                                             RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTV
                                                                                                                                                                                      QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
                                                                                                                                                                                                                                                                                    LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                                                                                                                                                               VLQPSGLYSLSSMVTV-PASSLSSKSYTCNVNHPATTTKVDKRVGTKTKPPCPICPACE-
DKASWQGGGIFQCAVMHEALHNHYTQKSISKTPG
                                                                                                                                                                QFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTREPQVYTLPPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----CPPCKCPAPNLLGGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWF
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                                        625
327
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A;Gene: IgG4
C;Superfamily: immunoglobulin C
F;82-151/Domain: immunoglobulin
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C;Genetics:
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R;Kacskovics, I.; Sun, J.; Butler, J.E.
R. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine
A;Reference number: I47158; MUID:95015845;
A;Accession: I47162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig gamma 4 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47162
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C;Superfamily: immunoglobulin C region; immunoglobulin
F;133-202/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG ident
A;Reference number: I47158; MUID:95015845; PMID:7930
A;Accession: I47159
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-277 < KAC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                          Matches
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                    475 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 534
                                                                                                                     416
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                                                                                                      -GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPGPSVFIFPPKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEE
                                                                            PGPSAFIFPPKPKDTLMISRTPKVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEEQ 123
                                                                                                                                                            VLQPSGLYSLSSMVTV-PASSLSSKSYTCNVNHPATTTKVDKRVGTKTKPPCPICPACEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 625
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FNSTYRVVSVLFIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTREPQVYTLPPPT 18:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RDELTKNOVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTV 591
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                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                        26.6%; Score 906.5; 63.4%; Pred. No. 1.2
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; Pred. No. 7.6e-47;
34; Mismatches 40
                                                                                                                                                                                                                                                                                                                  region; immunoglobulin homology <IMM>
                                                                                                                                                                                                                                        34;
                                                                                                                                                                                                                                        Mismatches
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A; Molecule type: protein
A; Residues: 4-68 <BIR>
R; Turner, K.J.; Cebra, J.J.
Biochemistry 10, 9-17, 1971
A; Title: Structure of heavy
A; Reference number: A90359; M
A; Accession: A90359
                                                                                                                                                                                                                         A; Molecule type: protein
A; Molecule type: protein
A; Residues: 227-311 <TR2>
R; Coliveira, B; Lamm, M.E.
Biochemistry 10, 26-31, 1971
A; Reference number: A90354; MUID:71058474; PMID:4922544
A; Centents: annotation; disulfide bonds
A; Mote: Cys-16 is involved in a heavy-light chain bond
A; Note: Cys-16; Cys-107, and Cys-110 form inter-heavy chain bonds
C; Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C; Complex: An immunoglobulin c region; immunoglobulin homology
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F; 21-81/Domain: immunoglobulin homology 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Trischmann, T.M.; Cebra, J.J.
Biochemistry 13, 4804-4811, 1974
A;Title: Primary structure of the C-H3 homology region from A;Reference number: A90385; MUID:75036073; PMID:4609467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 69-133;312-329 <TUR>
R;Tracey, D.E.; Cebra, J.J.
Biochemistry 13, 4796-4803, 1974
A;Title: Primary structure of the C-H2 homology region from A;Title: number: A90384; MUID:75036072; PMID:4429665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Birehtein, B.K.; Hussain, Q.Z.; Cebra, J.J.
Biochemistry 10, 18-25, 1971
A;Title: Structure of heavy chain from strain 13 guinea
A;Reference number: A90352; MUID:71058471; PMID:5538606
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G2GP
                                                                                             F;142-202/Disulfide bonds: #status experimental F;178/Binding site: carbohydrate (Asn) (covalen' F;248-308/Disulfide bonds: #status experimental
                                                                                                                                                               F;135-204/Domain: immunoglobulin homology <IM2>
F;241-310/Domain: immunoglobulin homology <IM3>
F;24-310/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein A; Residues: 134-226 < TRA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig gamma-2 chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Species: Cavia porcellus (guinea pig)
;Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 16-Jul-1999;Accession: A94553; A90352; A90359; A90384; A90385; A02151
                         Query Match
Best Local
  Matches
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  176;
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  Conservative
                         26.6%;
58.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chain from strain 13 guinea MUID:71058486; PMID:5538616
Pred. No. 1.56
l; Mismatches
                                             Score 906.5;
                                                                                                                         (covalent)
                         No. 1.5e-46;
                                                DB
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  57;
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change
C;Accession: I47158
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 133, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from t.
A;Reference number: I47158; MUID:9501845; PMID:7930579
A;Accession: I47158
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A;Cross-references: EMB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                            ;Superfamily: immunoglobulin C region; in
;133-202/Domain: immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                        Gene: IgG1
              26
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                                                                                                                         RDELTKNOVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTV
                                                                                                                                                                                                                        DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 625
                                                                                                                                                                   QFNSTYRVVSVLPIQHQDWLKGKEFKCKVNNVDLPAPITRTISKAIGQSREPQVYTLPPP
                                                                                                                                                                                    QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KVLPTWSTPVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD
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                                                                                                            AEELSRSKVTLTCLVIGFYPPDIHVEWKSNGQPEPENTYRTTPPQQDVDGTFFLYSKLAV
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                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                     26.1%; Score 891.5; DB 2; 62.8%; Pred. No. 1.2e-45;
                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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les 174; Conserv
350
                       640
                                                      290
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                          LDGLWTT 646
                                                      DGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGLDLDDICAEAKDGE
LDGLWTT 356
                                                                               DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGE
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A; Molecule type: DNA
A; Residues: 1-335, K' <YA2>
C; Comment: The semience of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 335-378 < ROS>
A; Residues: 335-378 < ROS>
A; Residues: 635-378 < ROS>
A; Residues: 635-378 < ROS>
A; Note: the translation of the first exon of the membrane-bound segment
B; Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;352-369/Domain: transmembrane #status predicted <TMM>F;370-405/Domain: intracellular #status predicted <INT>F;186/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Introns: 1/1; 98/1; 120/1; 230/1; 335/1; 378/3
C;Complex: An immunoglobulin heterotetramer subunit consists of two hain disulfide bonds. In some cases, such as IgA and IgW, the subunit C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Complete nucleotide sequence of immunoglobulin A;Reference number: A02157; MUID:80120716; PMID:6766534 A;Contents: a_allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell 26, 19-27, 1981
A;Title: Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma A;Reference number: A02158; MUID:82115295; PMID:6799207
A;Accession: A02158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Keywords: alternative splicing; duplication; glycoprotein; F;143-212/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Comment: The sequence of residues 1-334 was assumed to be identical with the correspon C;Comment: Cell lines producing IgG contain two mRNA species for Ig gamma chains. The ma hat it contains an alternative 3' end, encoded in separate exons, that is homologous wit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 335-405 <YAM>
A;Residues: 35-405 <YAM>
A;Cross-references: GB:J00462
R;Rogers, J.; Choi, E.; Souza,
                                                                                                                                                                                                                               110 PPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVN
                                 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
                                                                                                           GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
                                                                                                                                                                                                                                                                    DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                                                                                                                                                                                                                                                                                                                                                                                             LSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVEPKSC
                                                                                                                                                                                                                                                                                                                                                      VDKKLE-----PSGPISTINP-----C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PQALPQYAGSGNLTLALEA-----KTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLM
GLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PESVTVTWNSGSLSSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPAS-STT
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ilarity 47.4%;
Conservative 5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 884.5; DB 1;
Pred. No. 3.9e-45;
3; Mismatches 91;
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639

349

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A;Gene: Ig CH gamma-1
A;Introns: 98/1; 111/1; 221/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: 9lycoprotein; heterotetramer; immunoglobulin; membrane
F;161-225/Domain: immunoglobulin homology <IMM>
F;318/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Residues: 142-470 <SYM>
A;Residues: 145-470 <SYM>
A;Cross-references: EMBL:X16701
A;Note: the sequence was determined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440 R;Symons, D.B.A.; Clarkson, C.A.; Beale, D. Mol. Immunol. 26, 841-850, 198 A; Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and A;Reference number: S06610; MUID:90097956; PMID:2513487 A;Accession: S06610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Sanders, P.G. submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                           EKLTGSGELWWQAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALP 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKALEWVGGITSGGTTYYNPALKSRLSITKENSKSQVSLSVSSVTPEDTATYYCARSTYG 120
                                                                        PPELPGGPSVFIFPPKPKDTLTISGTPEVTCVVVDVGHDDPEVKFSWFVDDVEVNTATTK
                                                                                            APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 469
                                                                                                                                                                                                                                                                                                                                                                                                                      SVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IKILGNQGSFLTKGPSKLNDRADSRRSLWDQGN---FPLIIKNLKIEDSDTYIC----- 109
                           PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 529
                                                                                                                                                   KVDKAVDPT--
                                                                                                                                                                                       KVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVEPKSCDKTHTCPPCP 409
                                                                                                                                                                                                                                                                QYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVGD----
PREEQFNSTYRVVSALRIQHQDWTGGKEFKCKVHNEGLPAPIVRTISRTKGPAREPQVYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLWTLLFVLSAPIGVLSQVQLRESGPSLV--KPSQTLSLTCTVSGFSLSSYALTWVRQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFRHLLLVLQ----LALLPAATQGNKVVLGKKGDTVELTCTAS--QKKSIQFHWKNSNQ
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35.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 884.5; DB 2
Pred. No. 4.8e-45;
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A;Cross-references: EMBL:X69797 C;Superfamily: immunoglobulin C;Keywords: immunoglobulin F;277-346/Domain: immunoglobulin

immunoglobulin homology <IMM;

region; immunoglobulin

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-472 <PAT>

R;Patri, S.; Nau, F. submitted to the EMBL Data Library, A;Reference number: S31459
A;Accession: S31459

December

Ig gamma-1 chain - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis
C;Date: 13-Jan-1995 #sequence_revision

ammon aries 13-Jan-1995

#text_change 16-Jul-1999

Accession: S31459

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A;Gene: IgG3
C;Superfamily: immunoglobulin C region; immunoglobulin F;133-202/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Five putative subclasses of swine IgG identified A; Reference number: I47158; MUID:95015845; PMID:7930579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: I47161
R; Kacskovics, I.; S
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A; Residues: 1-328 < KAC>
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                                                                                                                                                                                                                                                                                                                                                                                         ocal Similarity
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l. 153, 3565-3573, 1994
                                                                         234
                                                                                                                                                 174
                                                                                                                                                                                    474
                                                                                                                                                                                                                         114
                                                                                                                                                                                                                                            414 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   530 LPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOP--ENNYKTTPPVLDSDGSFFLYS
                                                                                                                                                                                                                                                                                                                                   371 LLSDSGQVLLESNIKVLPTWSTPVEPKSCDKTH------TCPPCPAPEL
                                                                                                                                                                                                                                                                                                                                                                          170;
                                                                                                                                                                      QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
                                                                                                                                                                                                                       VAGPSVFIFPPKPKDTLMISQTPEVTCVVVDVSKEHAEVQFSWYVDGVEVHTAETRPKEE
                 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 625
                                                                       AEELSRSKVTVTCLVIGFYPPDIHVEWKSNGQPEPEGNYRTTPPQQDVDGTFFLYSKLAV
                                                                                                        RDELTKNOVSLTCLVKGFYPSDIAVEWESNGQ---PENNYKTTPPVLDSDGSFFLYSKLTV 591
                                                                                                                                                                                                                                                                                                VLQPSGLYSLSSMVTV-PASSLSSKSYTCNVNHPATTTKVDKRVGTKTKPPCPICPGCE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAPPQEELSKSTVSLTCMVTSFYPDYIAVEWQRNGQPESEDKYGTTPPQLDADSSYFLYS
DKARWDHGETFECAVMHEALHNHYTQKSISKTQG
                                                                                                                                                 QFNSTYRVVSVLPIQHQDWLKGKEFKCKVNNVDLPAPITRTISKAIGQSREPQVYTLPPP
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                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL: U03781; NID: g433127; PIDN: AAA52219.1; PID: g433128
                                                                                                                                                                                                                                                                                                                                                                                         25.9%;
                                                                                                                                                                                                                                                                                                                                                                          32;
                                                                                                                                                                                                                                                                                                                                                                      Score 883.5; DB 2;
Pred. No. 3.4e-45;
2; Mismatches 51;
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a 81

Similarity

Length

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Ig heavy chain C region - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Bate: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-
C;Accession: C30554
R;Foley, R.C.; Beh, K.J.
J. Immunol. 142, 708-711, 1989
A;Title: Isolation and sequence of sheep Ig H and L chain cDNA.
A;Reference number: A30554; MUID:8903962; PMID:2492052
A;Accession: C30554
A;Status: preliminary; not compared with conceptual translation
A;Residues: 1-308 <FOL>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology <IMM>
F;113-182/Domain: immunoglobulin homology <IMM>
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Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
Date: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-
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Best Local S
Matches 209
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Best Local Similarity
Matches 161; Conserv
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EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
                                                                                                                                                               ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
                                                                                                                                                                                                                                      ILQSSGLYSL-SSVVTVPASTSGAQTFICNVAHPASSTKVDKRVEPGCPDPCKHCRCPPP
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                                                                                                                                                                                                                                                                                                                                                                38; Mismatches
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Pred. No. 1.2e-43;
5; Mismatches 143
                                                                                                                                                                                                                                                                                                                                                                                              Score 851; DB 2;
Pred. No. 2.7e-43;
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Gene 74, 473-482, 1988 A;Title: Evolution of the ra A;Reference number: PS0017;

rat immunoglobulin gamma heavy-chain 7; MUID:89232738; PMID:3149946

gene

family

R; Brueggemann,

Ig gamma-2b chain C region - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 C;Accession: PS0018; B25941

#text_change

16-Jul-1999

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A;Introns: 97/1; 113/1; 223/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap c;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology (Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobu r;19-83/Domain: immunoglobulin homology (IM1)
F;97-112/Region: hinge
F;136-205/Domain: immunoglobulin homology (IM2)
F;242-309/Domain: immunoglobulin homology (IM3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Wels, J.A.; Word, C.J.; Rimm, D.; Der-Balan, G.P.; Max
EMBO J. 3, 2041-2046, 1984
A;Title: Structure analysis of the murine IgG3 constant
A;Reference number: A02156; MUID:85027161; PMID:6092053
A;Accession: B02156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-329 <WEL>
A; Cross-references: GB: J00451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig gamma-3 chain C region, secreted form - mouse C;Species: Mus musculus (house mouse) C;Date: 17-Mar-1997 #sequence_revision 31-Mar-1991
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PS0018
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Best Local S
Matches 154
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-309/Domain: immunoglobulin homology <IM3>
-322/Binding site: carbohydrate (Asn) (cov
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                                                                                               VFSCSVMHEALHNHYTQKSLSLSPG 625
                                                                                                                                                     QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
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                                                                              IFTCSVVHEALHNHHTQKNLSRSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.9%; Score 849.5; DB 1
58.1%; Pred. No. 3.5e-43;
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monocional antibody 13-1 heavy chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C;Accession: PC4436
R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Hara Biochem. Biophys. Res. Commun. 240, 565-572, 1997
A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a p A;Reference number: JC5810; MUID:98063277; PMID:9398605
A;Molecule type: protein
A;Residues: 1-444 AKA>
C;Comment: This catalytic antibody has peroxidase oxidase activity. It is directed C;Superfamily: immunoglobulin cregion; immunoglobulin homology
F;251-320/Domath: immunoglobulin homology < TMM>
F;22/Disulfide bonds: interchain (to 98) #status predicted
F;99/Disulfide bonds: interchain (to 109) #status predicted
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C;Superfamily: immunoglobulin C region; immuno
C;Keywords: immunoglobulin
F;20-82/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-33 <BRU>
R;Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, S.; Waldmann, H. Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986
Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986
A;Title: Immunoglobulin heavy chain locus of the rat: striking homology to mouse A;Reference number: A25941; MUID:86287397; PMID:3016742
A;Accession: B25941
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A;Molecule type: DNA
A;Residues: 227-333 <BR2>
C;Genetics:
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                                                        PASSTKVDKKIVPRDCGCKPCICTVPEV---SVFIFPPKPKDVLTITLTPKVTCVVVDI
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    SKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSA
                                                                                PTWSTPVEPKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 445
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61.7%;
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Pred. No. 2e-4
14; Mismatches
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Pred. No. 7.6e-43;
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YTQKSLSLSPG
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-469 < DUC>
A;Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;276-345/Domain: immunoglobulin
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C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995
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les 216; Conserv
                                                                                                                                                                                                                               TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN 494
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DIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNH
                                           DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH
                                                                                                                                             GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS
                                                                                                                                                                                             SPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMS
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Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986
A;Title: Immunoglobulin heavy chain locus of the rat: striking homo A;Accession: C25941
A;Accession: C25941
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 220-326 <BR2>
C;Genetics: 99/1; 113/1; 220/1
C;Superfamily: immunoglobuli-
C;Keywords: immunoglobuli-
C;Keywords: immunoglobuli-
C;Keywords: immunoglobuli-
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C;Date: 07-Jun-1
C;Accession: PS(
R;Brueggemann, !
                                                                      Ig gamma-1 chain C region, secreted form - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1980 #sequence_revision 24-Sep-1981 #text_change 16-Jul-1999
C;Accession: A02159; A26234; A26236
C;Accession: A02159; A26234; A26236
R;Honjo, T.; Obats, M.; Yamawaki-Kataoka, Y.; Kataoka, T.; Kawakami, T.; Tak
Cell 18, 559-568, 1979
A;Title: Cloning and complete nucleotide sequence of mouse immunoglobulin ga
A;Reference number: A02159; MUID:80045036; PMID:115593
A;Accession: A02159
A;Molecule type: DNA
A;Residues: 1-324 <HON>
A;Conse-references: GB:000453
A;Conse-references: GB:000453
A;Conse-references: GB:000453
A;Conse-references: GB:000453
A;Conse-references: GB:000453
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A;Title: Evolution of the rat immunoglobulin gamma heavy-chain A;Reference number: PS0017; MUID:89232738; PMID:3149946
A;Accession: PS0017
A;Molecule type: DNA
A;Residues: 1-326 <BRU>
R;Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold,
A;Note: the sequence was determined from the germline gene A;Note: Lys-324 is removed posttranslationally R;Obsta M.; Yamawaki-Kataoka, Y.; Takahashi, N.; Kataoka, Gene 9, 87-97, 1980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKWQQGNTFTCSVLHEGLHNHHTEKSLSHSPG
                                                                                                                                                                                                                                                                                                                                                                                                                           SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEEMTQNEVSITCMVKGFYPPDIYVEWQMNGQPQENYKNTPPTMDTDGSYFLYSKLNVKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGQVLLESNIKVLPTWSTPVEPKSCDKTH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGLYTLTSSVTV-PSSTWPSQTVTCNVAHPASSTKVDKKIVPRNCGGDCKPC----ICTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTTKSFSRTPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 828; DB 2;
Pred. No. 6.6e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #text_change 16-Jul-1999
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                  Shimizu,
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                                                                                                                                                                                                                    T.; Takahashi,
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A; Molecule type: mRNA A; Residues: 1-329 < BRU>

A; Cross-references: EMBL:X07189;

NID: 957602; PIDN: CAA30169.1;

PID:g663228

R;Brueggemann, M.; Delmastro-Galfre, P.; Waldmann, H.; C:Eur. J. Immunol. 18, 317-319, 1988
A;Title: Sequence of a rat immunoglobulin gamma-2c heavy
A;Reference number: S00847; MUID:88166903; PMID:3127222
A;Accession: S00847

Ig gamma-2c chain C region - rat (fragment)
c;Species: Rattus norvegicus (Norway rat)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 23-Jul-1999
C;Accession: S00847

H.; Calabi,

chain

constant region

CDNA:

ext

S00847

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J. Biol. Chem. 253, 6068-6075, 1978
A;Title: Evolution of immunoglobulin subclasses. Primary structure of a murine myeloma g A;Reference number: A26237; MUID:78242288; PMID:98524
A;Contents: annotation; MOPC 21
A;Note: this is the final paper in a series reporting the protein sequence, the disulfid A;Note: there are a number of differences from the sequence shown
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Complex: An immunoglobulin heterotetramer subunit consists of two ide hain disulfide bonds. In some cases, such as IgA and IgM, the subunits C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Rogers, J.; Clarke, P.; Salser, W.
Nucleic Acids Res. 6, 3305-3321, 1979
A;Title: Sequence analysis of cloned cDNA encoding part
A;Reference number: A26236; MUID:80012837; PMID:113776
A;Contents: MOPC 21
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F;237-304/Domain: immunoglobulin homology <1M2>
F;237-304/Domain: immunoglobulin homology <1M2>
F;237-304/Domain: immunoglobulin homology <1M2>
F;237-82,138-198,244-302/Disulfide bonds: #status experimental
F;102/Disulfide bonds: interchain (to light chain) #status experimental
F;104,107,109/Disulfide bonds: interchain (to heavy chain) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;20-84/Domain: immunoglobulin homology <IM1>
F;98-110/Region: hinge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 170-275,'D',277,'D',279-322 <ROG>
A;Cross-references: GB:V00795; NID:g51830; PIDN:CAA24176.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 76-324 <OBA>
A;Cross-references: GB:V00775; NID:g51652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A; Contents: MOPC 310
                                                                                                                                                                                                                                                                                                                                                                          S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A26236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;174/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
     264
                                                                                                                                                                                                                     144
                                                                                                                                                                                                                                                                                                                                                                                     388
                                                                                                                                                                                                                                                                                                                                                                                                                                        144;
                                                                                                                                                                                                                                                                                                                                87
PAENYKNTOPIMNTNGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPG
                                                                                                                                         ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ
                                       PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                             AFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQ
                                                                                                                                                                                                                     SKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSA
                                                                                                                                                                                                                                                                     SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
                                                                                                                                                                                                                                                                                                                        PASSTKVDKKIVPRDCGCKPCICTVPEV---SSVFIFPFKPKDVLTITLTPKVTCVVVDI
                                                                                                                                                                                                                                                                                                                                                                                PTWSTPVEPKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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_A26234; MUID:80202559; PMID:6769752
                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 826.5; DB 1;
Pred. No. 8e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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F;142-211/Domain: immunoglobulin homology <IM2>
F;248-315/Domain: immunoglobulin homology <IM3>
F;15/Disulfide bonds: interchain (to light chain) #status predicted
F;27-82,149-209,255-313/pisulfide bonds: #status predicted
F;108,117/Disulfide bonds: interchain (to heavy chain) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Residues: 118-267, 'E',269-328, 'G',330-334 <DOG>
A;Residues: 118-267, 'E',269-328, 'G',330-334 <DOG>
C;Comment: Lys-335 is removed posttranslationally.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap c;Complex: An immunoglobulin heterotetramer subunit and IgM, the subunits associate into la c;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin p;20-84/Domain: immunoglobulin homology <IMl>
F;98.118/Region: hinge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Experimental source: strain C57BL/6
R;Dognin, M.J.; Lauwereys, M.; Strosberg, A.D.
Proc. Natl. Acad. Sci. U.S.A. 78, 4031-4035, 1981
A;Title: Multiple amino acid substitutions between murine
A;Reference number: A32656; MUID:82037777; PMID:6794027
A;Accession: A32656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig gamma-2a chain C region, secreted form (allele b) - mouse (Species: Mus musculus (house mouse) C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999 C;Accession: A02153; A32656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: immunoglobulin F;20-84/Domain: immunoglobulin homology <IMM>
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A;Title: Multiple differences between the nucleic acid sequences
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A;Accession: A02153
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A; Residues: 1-335 <SCH>
                                                                                                                                                                                                                                                 185/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                        Matches
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                                                                                                                                                        Similarity
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                                                            PQALPQYAGSGNLTLALEA-----KTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLM 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGRPSVFIFPPKPKDILMITLTPKVTCVVVDVSEEEPDVQFSWFVDNVRVFTAQTQPHEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REQMSKNKVSLTCMVTSFYPASISVEWERNGELEQDYKNTLPVLDSDESYFLYSKLSVDT
      PEPVTLTWNSGSLSSGVHTFPALLQSGLYTLSSSVTVTSNTWPSQTITCNVAHPAS----
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55.9%; Pred. No. 2.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUID:82037861; PMID:6170065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46;
                                                                                                                        Score 816; DB 1;
Pred. No. 3.5e-41;
2; Mismatches 86
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                                                                                                                           Indels
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      68
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A;Introns: 1/1; 98/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associst; Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; if;20-84/Domain: immunoglobulin homology <IMI>
                                                                                                                                                                                                                                                                                                                                                      A;Note: The sequence was determined from the germline gene
A;Note: Lys-330 is removed posttranslationally
R;Bourgois, A.; Fougereau, M.; Rocca-Serra, J.
Bur. J. Biochem. 43, 423-435, 1974
A;Title: Determination of the primary structure of a mouse IgG2a immunoglobulin: amino-ac
A;Reference number: A32659; MUID:74175517; PMID:4831970
A;Contents: annotation; myeloma protein MOPC 173
A;Note: this is one paper in a series reporting the sequence; for additional references,
A;Note: this sequence differs from that shown at a number of positions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Note: the sequence was determined from the germline gene R;0110, R.; Auffray, C.; Morchamps, C.; Rougeon, F. Proc. Natl. Acad. Sci. U.S.A. 78, 2442-245.

Proc. Natl. Acad. Sci. U.S.A. 78, 2442-245.

A;Title: Comparison of mouse immunoglobulin gamma-2A and gamma-2B chain genes suggests A;Reference number: A32658; MUID:81223894; PMID:6787604

A;Accession: A32658
                                                                                                                                                                                                                                          R;de Preval, C.; Fougereau, M.
Eur. J. Blochem. 30, 452-462, 1972
Fur. J. Blochem. 30, 452-462, 1972
A;Tille: Determination of the primary structure of a mouse gammaG2a immunoglobulin. Ident A;Reference number: A32660; MUID:73056887; PMID:4565406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-330 <OLL>
                                                                                                                                                                           C;Genetics:
                                                                                                                                                                                                                 A; Contents:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; MOLECULE TYPE: DNA
A; Residues: 1-330 < YAM>
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annotation;

MOPC

disulfide

pouga

l light (kapr immunoglobu

Ş	340 LSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVEPKSC 399
₽b O	90STKVDKKIEPRVPITQNPC 108
Ş	400 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 459
Вb	109 PPHQRVPPCAAPDLLGGPSVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDPDVQISWFVN 168
Ś	460 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 519
В	169 NVEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNRALPSPIEKTISKPR 228
Qy	520 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 579
g	229 GPVRAPQVYVLPPPAEEMTKKEFSLTCMITGFLPAEIAVDWTSNGRTEQNYKNTATVLDS 288
δ	580 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 625
₽ B	289 DGSYFMYSKLRVQKSTWERGSLFACSVVHEVLHNHLTTKTISRSLG 334
RESULT 39 G2MSA	
Ig gamma-	Ig gamma-2a chain C region, secreted form (allele a) - mouse Cr.Species: Mus musculus (house mouse)
C;Date: 3 C;Accessi	C;Decres: Mus musculus mouse mouse; C;Date: 30-Sep-1980 #sequence revision 01-Sep-1981 #text_change 16-Jun-2000 C;Accession: A02152; A32657; A32658
R;Sikorav Nucleic A	, J.L.; Auffray, C.; Rougeon, F. cids Res. 8, 3143-3155, 1980
A;Title: A;Referen	A;Title: Structure of the constant and 3' untranslated regions of the murine Balb/C A;Reference number: A02152; MUID:81076554; PMID:6777755
A; Molecul	A;Accession: A02152 A;Molecule type: mRNA
A; Kesique A; Cross-r	A;Resiques: 1-330 <sik> A;Cross-references: GB:V00798; NID:q51835; PIDN:CAA24178.1; PID:q1333984</sik>
R;Yamawak	R;Yamawaki-Kataoka, Y.; Miyata, T.; Honjo, T.
A;Title:	U
A; Accessi	A; Reference number: A3265/; MOID:811989/6; PMID:6262/29 A;Accession: A3265/

gamma

evo]

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A; Molecule type: DNA
A; Residues: 138-161,'L',163-189,'FP',193-474 < YAM>
A; Residues: 138-161,'L',163-189,'FP',193-474 < YAM>
A; Cross-references: GB:JO0461
A; Note: the sequence was determined from the germline gene
R; Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 206, 1299-1303, 1979
A; Title: Structure of the constant and 3' untranslated regions of
A; Reference number: A26235; MUID:80081501; PMID:117548
A; Contents: MPC 11
A; Accession: A26235
A; Molecule type: mRNA
A; Residues: 138-172,'P', 174-189,'FP', 193-376,'T', 378-474 < TU1>
A; Note: Lys-474 is probably removed posttranslationally
R; Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F
Science 206, 1303-1306, 1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig gamma-2b chain - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1980 #sequence revision 01-Dec-2000 #text change 01-Dec-2000 C;Accession: $25057; A02157; A26235; A26232; A26233; A53598
R;Fischer, R; Voss, A; Niersbach, M; Munziker, W; Hirsch, H.J.; Kreuzald submitted to the EMBL Data Library, July 1992
A;Bescription: Production of a Tobacco mosaic virus (TMV) inactivating neoto A;Reference number: $25057
A;Accession: $25057
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                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Complete nucleotide sequence of immunoglobulin A;Reference number: A02157; MUID:80120716; PMID:6766534 A;Contents: a allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X67210; NID:g54826; PIDN:CAA47649.1; 1
R;Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.;
Nature 283, 786-789, 1980
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A; Residues: 1-474 <FIS>
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;243-310/Domain: immunoglobulin homology <IM3>
;15/Disulfide bonds: interchain (to light chain) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-82,144-204,250-308/Disulfide bonds: #status experimental 107,110,112/Disulfide bonds: interchain (to heavy chain) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPG
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Pred. No. 4.2e-41;
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; Honjo, T.
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F;281-350/Domain: immunoglobulin homology <IM2>
F;387-454/Domain: immunoglobulin homology <IM3>
F;387-454/Domain: immunoglobulin homology <IM3>
F;152/Disulfide bonds: interchain (to light chain) #status predicted
F;164-220,288-348,394-452/Disulfide bonds: #status predicted
F;247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status
F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Introns: 138/1; 236/1; 258/1; 368/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein A; Residues: 234-251 <KIM>C; Comment: The a allele so
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J. Biol Chem. 269, 12345-12350, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 138-161,'L',163-189,'FP',193-300,'R',302-331,'A',333-437,'DI',440-474
A;Cross-references: GB:J00461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A26233
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Nature 296, 761-763, 1982
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A;Residues: 138-172,'P',174-189,'FP',193-376,'T'
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                                                                                          NIKVLPTWSTPVEPKSCDKTHTCPPCPAPELLGGPSVFLPPPKFKDTLMISRTPEVTCVV
VDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKV
                        VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV
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                                                                                                                                                                                      SQTVTCSVAHPAS-STTVDKKLE-----PSGPISTINP--
                                                                                                                                                                                                                                     QKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLES
                                                                                                                                                                                                                                                                                                                               VKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQL
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A;Map position: 12
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Superfamily: immunoglobulin C region; immunoglobulin; pyroglutamic acid
C;Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F;1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F;1-11/Domain: V-D-J region <CMP>
F;118-446/Domain: C region <CH1>
F;215-230/Region: hinge
F;231-340/Domain: C2 region <CH2>
F;231-340/Domain: C3 region <CH3>
F;341-446/Domain: C3 region <CH3>
F;341-446/Domain: immunoglobulin homology <IMM>
F;247/Domain: immunoglobulin homology <IMM>
F;2-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F;2-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F;2-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F;2-97/Binding site: carbohydrate (Asn) (covalent) #status experimental
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R;Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bsubmitted to the EMBL Data Library, January 1993
A;Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against
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C;Species: Mus musculus (house mouse)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
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A; Accession: S40295
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                                      VVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSD
                                                                                                                                                                                                                                                             QGTSVTVSSAKTTAPSVYPLAP----VCGDTT----
                                                                                                                                                                                                                                                                                                      QSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFK 196
                                                                                                                                                                                                                                                                                                                                                   GKATLTVDTSSSTAYMQLSSLTSEDSAVYFC------
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                                                                                                                           KNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQ--YAGSGNLTLALEAKTGKLHQEVNL
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-VTSSTWPSQSITCNVAHPAS---
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Pred. No. 1
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Ig gamma-2a chai
C;Species: Rattı
C;Date: 07-Jun-1
C;Dacession: PSI
R;Brueggemann, 1
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A;Title: Immunoglobulin heavy chain locus of the rat: striking A;Reference number: A25941; MUID:86287397; PMID:3016742
A;Accession: D25941
A;Status: preliminary
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A;Title: Evolution of the ra
A;Reference number: PS0017;
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A; Residues: 216-322 <BR2>
C; Genetics:
A; Introns: 98/1; 109/1; 2
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A; Residues: 1-322 < BRU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g gamma-2a chain C region - rat
;Species: Rattus norvegicus (Norway rat)
Date: 07-Jun-1990 #sequence_revision 07
;Accession: PS0019; D25941
                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74, 473-482, 1988
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                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                         FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 479
                                                               SQVSITCMVKGFYPPDIYTEWKMNGQPQENYKNTPPTMDTDGSYFLYSKLNVKKETWQQG
                                                                                   NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 599
                                                                                                                                                        RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 539
                                                                                                                                                                                                  FIFPEKTKDVLTITLTPKVTCVVVDISQNDPEVRFSWFIDDVEVHTAQTHAPEKQSNSTL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFM
NTFTCSVLHEGLHNHHTEKSLSHSPG
                              NVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                    RSVSELPIVHRDWLNGKTFKCKVNSGAFPAPIEKSISKPEGTPRGPQVYTMAPPKEEMTQ
                                                                                                                                                                                                                                                                       SGLYTLTSSVTVPSSTWSSQAVTCNVAHPASSTKVDKKIVPRECNPCGCTGSEV---SSV
                                                                                                                                                                                                                                                                                                       SGQVLLESNIKV-LPTWST-----PVEPKSCDK---THTCPP--CPAPELLGGPSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NHHTTKSFSRTPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NHYTOKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVWHEALH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LNGKEYKCKVSNKALPAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLSPMVTCVVVDVSEDDPDVQISWFVNNVEVLTAQTQTHREDYNSTLRVVSALPIQHQDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGQVLLESNIKVLPTWSTPVEPKSCDKTHTCPP---CPAPELLGGPSVFLFPPKPKDTLMI
                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              216/1
                                                                                                                                                                                                                                                                                                                                                         23.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rat immunoglobulin gamma heavy-chain 7; MUID:89232738; PMID:3149946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            446
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9
                                                                                                                                                                                                                                                                                                                                         Score 795; DB
Pred. No. 5.8e
39; Mismatches
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321
                               625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibody
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gamm

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Ig gamma-2b chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Species: Nus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C;Accession: S01321
R;de Waele, P:, Feys, V:, van de Voorde, A:, Molemans, F:, Fiers, W.
Rur: J. Biochem. 176, 287-295, 1988
A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed a A;Reference number: S01320; MUID:88329081; PMID:3138116
A;Accession: S01321
A;Molecule type: mRNA
A;Residues: 1-475 <DE1>
A;Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781
A;Note: this sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: Immunoglobulin C region; immunoglobulin homology
F;1-19/Domain: signal sequence #status predicted <MAT>
F;1-59-223/Domain: immunoglobulin homology <IMM>
RESULT
S06611
Ig gamm
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    gamma-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 LTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKID 198
    chain C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 LGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKILGNQG-----SFLTKGPSKLNDRAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205/
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                                                                                                 TISRSPG
                                                                                                                                                                                                                                                                                                                                                        TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
                                                                                                                                          SLSLSPG
                                                                                                                                                                                                       EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK 618
                                                                                                                                                                                                                                                                                KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
                                                                                                                                                                                                                                                                                                                                   TCVVVDVSEDDPDVQISWFVNNVEVLTAQTQTHREDYNSTIRVVSALPIQHQDWMSGKEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STWPSQTVTCSVAHPAS-----STTVDKKLEP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKATLTVDKSSSTAYLHLSSLTSEDSAVYFCA---GPRQVGLLPFG-----YWGQG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRRSLW----DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQS
                                                                                                                                                                             EWTSNGHTEENYKDTAPVLDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKK
                                                                                                                                                                                                                                                          KCKVNNKDLPAPIERTISKIKGIVRAPQVYILSPPPEQLSRKDVSLTCLAVGFSPEDISV
                                                                                                                                                                                                                                                                                                                                                                                                                   ----PT--STINP--CPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLESNIKVLPTWSTPVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQV 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----QSGLYTMSSSVTVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LARPGASVKLSCKASGYTLTSYGISW-----VKQRTGQGLEWIGEIYPGSGNSYFNEKFK
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    region
                                                                                                                                          625
                                                                                                     474
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    (clone 32.2)
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7; Mismatches
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    bovine (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162;
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C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Feb-1990 #sequence revision 28-Feb-1990 #text_change 16-Jul-1999
C;Accession: S06611; B31303
R;Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A;Title: Structure of bovine immunoglobulin constant region heavy chain gamu A;Reference number: S06610; MUID:90097956; PMID:2513487
A;Accession: S06611.
                                                                                                                                                                                                                                                                                                                                                                                 R;Heidmann, O.; Rougeon, F.
Nucleic Acids Res. 10, 1535-1545, 1982
A;Title: Molecular cloning of rabbit gamma
A;Reference number: 146732; MUID:82174328;
A;Accession: 146732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X16702
A;Note: the sequence was determined from the germline gene C;Genetics:
A;Genetics:
A;Gene: Ig CH gamma 2
A;Introns: 99/1; 112/1; 219/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Superfamily: immunoglobulin C region; membrane protein F;20-85/Domain: immunoglobulin homology <IMM>
F;175/Binding site: carbohydrate (Asn) (covalent) #status predicted
                         S
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                                                                                                                                                                                                                                                A;Cross-references: GB:J00665; NID:g165109; PIDN:AAA31288.1; PID:g165110 C;Superfamily: immunoglobulin C region; immunoglobulin homology F;93-160/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-180 < HEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig gamma heavy chain constant region - rabbit (fragment)
c;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 21-Jan-2000
C;Accession: I46732
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A; Residues: 1-327 <SYM>
                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                Query Match
Best Local S
Matches 124
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Best Local S
Matches 148
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                                                                                                                                                                                       Local Similarity
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                              808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPSVPIFPPKPKDTLMITGTPEVTCVVVNVGHDNPEVQFSWFVDDVEVHTARTKPREEQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NSWQRGDTYTCVVMHEALHNHYMQKSTSKSAG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELTKNQVSLTCLVKGFYPSDIAVEWESNCQ--PENNYKTTPPVLDSDGSFFLYSKLTVDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLQSSGLYSLSSMVTV-PASSSGTQTFTCNVAHPASSTKVDKAVGVSSDCSKPNNQHCVR
                                                                         DDPEVQFTWYINNEQVRTARPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKAL
                                                                                                                   EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELSKSTVSLTCMVIGFYPEDVDVEWQRDRQTESEDKYRTTPPQLDADRSYFLYSKLRVDR
                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.7%;
                                                                                                                                                           20.6%; Score 702; DB 2; 69.7%; Pred. No. 8.7e-35; tive 26; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1e-3
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 774; DB 2; Length 327; Pred. No. 1e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                heavy chain
PMID:6280149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64;
                                                                                                                                                                                                        Length 180
                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA.
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                                                                                                                                                                Gaps
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                                                                           61
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A; Molecule type: mRNA
A; Residues: 1-249 < KHA>
A; Cross-references: EMBL: X81696
C; Superfamily: immunoglobulin C
F; 162-229/Domain: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Paccession: S69340
C; Accession: S69340
C; Accession: S69340
R; Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
R; Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
R; Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Rur. J. Biochem. 229, 54-60, 1995
Bur. J. Biochem. 229, 54-60, 1995
Bur. J. Biochem. 229, 54-60, 1995
Bur. J. L.; Cogne, M.
Richamlichi, A.A.; Alexandrian disease.
A; Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A; Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A; Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A; Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain VHIII-D-JH-CH3 region - human
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  á
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A36040
A36040
Ig heavy chain V-III region (ART) - human (fragments)
C;Species: Homo sapiens (man)
C;Date: 16-Nov-1990 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     á
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                        Superfamily: immunoglobulin C region; immunoglobulin homology;162-229/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                     Local Sim
hes 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.8%;
al Similarity 77.5%;
110; Conservative
                                                      125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        604 CSVMHEALHNHYTQKSLSLSPG 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137
                                                                                                                                                                                                              460 GVEVHNAKTKPREEQYNSTYRVVSVLT-------VLHQDWLNGKEYKCKVSN 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                484 VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVS 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 VAAALLTDWGQG------TLVTVSSGQPREPQVYTLPPSRDELTKNQVS 136
                                                                                                                                                                                                                                                                     h 16.8%;
Similarity 62.9%;
17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS 603
                                                                                                     KALPAPIE----KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
                                                      -- LPSAIHFWGQGTRVIVSSGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
                                                                                                                                                            GDSVRGRFTISRDNSENQLYLQMNSLTAEDTAVYYCAKDVGSVIH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSVMHEGLHNHYTQKSLSLSPG 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAPIEKTISKARGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAE 121
                                                                                                                                                                                                                                                                  Score 572.5; DB 2; Length 249; Pred. No. 6.1e-27; 9; Mismatches 23; Indels 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 574.5; DB 2;
Pred. No. 3.9e-27;
3; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                     37;
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                                                      182
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C;Superfamily: ir C;Keywords: immur F;37-120/Domain:
                                                                                                                                                                                                                                                                                                                                                                                               N;Alternate names: Ig gamma chain (7.8S)
N;Alternate names: Ig gamma chain (7.8S)
C;Species: Anas platyrhynchos (domestic duck)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: B46529; S20759
R;Magor, K.E.; Warr, G.W.; Middleton, D.; Wilson, M.R.; Higgins, D.A.
J.Immunol. 149, 2627-2633, 1992
A;Title: Structural relationship between the two IgY of the duck, Anas platyrhynchos: mol A;Reference number: A46529; MUID:93017865; PMID:1401901
A;Accession: B46529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, Eur. J. Biochem. 192, 767-775, 1990
A;Title: Construction and characterization of a recombinant murine monoclon. A;Reference number: S14236; MUID:91006173; PMID:2209622
A;Accession: S14236
                                                                                                                                                                                                          A;Note: sequence extracted from NCBI backbone (NCBIP:116127) C;Superfamily: immunoglobulin C region; immunoglobulin homol C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X56393; NID:g51617; PIDN:CAA39804.1; PID:g51618 C;Superfamily: immunoglobulin c region; immunoglobulin homology C;Keywords: immunoglobulin C;Keywords: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X65219; NID:g62442; PIDN:CAA46322.1; A;Experimental source: spleen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S14236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig gamma-1 chain C region (15C5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ś
                                           á
                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-572 < MAG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig Y heavy chain (7.8S) - duck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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A; Residues: 1-152 < VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               535 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       475 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQQPREPQVYTLPPSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             620 LSLSPG
                                              150 SPSVQCRSPRGKNI-QGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLAFQKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NWEAGNTFTCSVLHEGLHNHHTEKSLSHSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQMAKDKVSLTCMITDFFPEDITVEWQMNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSLSPG
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  APAVKGRFTISRNNGQSTATLQMNSLKAEDTATYYCA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                    immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                625
                                                                                                                11.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33;
                                                                                       Score 394.5; DB 2;
Pred. No. 6.1e-16;
0; Mismatches 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 566; DB 2;
Pred. No. 7.9e-27;
3; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                            Indels 109;
                                                                                                                                      Length 572;
                                                                                                                                                                                                                                                                                                          PID:g62443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>.</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                          Gaps
    RSS
    129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242
                                                   208
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                                                                                            22
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RESULT 50 \$1468] 19 mm chain precursor, membrane-bound (clone 201) - human C;species; Komo sapiens (man) C;species; Komo sapiens (man) C;species; Romo sapiens (man) C;species; Romo sapiens (man) C;species; Romo sapiens (man) C;species; Sides; Sosdaf C;species; Sides; Sides C;species; Sides; Milb:90332450; pmiD:211596 C;species; Sides; Milb:90332450; pmiD:211596 C;species; Sides; Sides; Milb:90332450; pmiD:211596 C;species; Sides; Sides; Milb:90332450; pmiD:211596 C;species; Sides; Milb:90332450; pmiD:211596 C;speci	OY 209 SIVYKKEGEOVEPSFPLAFTVEKLTGS
RESULT 51 So4845 Ig heavy chain precursor - African clawed frog (fragment) C;Species: Xenopus laevis (African clawed frog) C;Species: Xenopus laevis (African clawed frog) C;Species: Xenopus laevis (African clawed frog) C;Date: 12-Peb-1993 #sequence_revision 12-Peb-1993 #text_change 26-Aug-1999 C;Accession: 804845; MOS695 C;Accession: So4845; MID: 818, 1999 A,Title: Nucleotide sequence of a cDNA encoding a third distinct Xenopus immunoglobulin A;Accession: 804845; MUID: 89345103; PMID: 2503814 A;Accession: 804845; MUID: 89345103; PMID: 2503814 A;Accession: 804845; MUID: 89345103; PMID: 2503814 A;Accession: 805695 A;Ac	Qy 203 AFQKASSIVYKKBGEQVEFSPELAFTVEKLTGSGELMWQAERASSSKSWITFDLK 257

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Ig mu chain C region, member of the control of the 
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                                                                                                                                                                                                                                           C;Complex: An immunoglobulin heterotetramer subunit consists of two identical lighal disulfide bonds. In some cases, such as IgA and IgM, the subunits associate C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin homology
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hain
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A;Mccession: A37517
A;Mcsidues: 410-476 <ROG>
A;Cross-references: GB:V00821; NID:g52355; PIDN:CAA24202.1; PIR:CAA24202.1; 
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A;Cross-references: GB:V00816; GB:J00444; NID:g52343; PIDN:CAA24197.1; PID:g5A;Cross-references: GB:V00816; Carter, C.; Calame, K.; Bond, M.; Hood, L.; Wall, R. R;Rogers, J.; Early, P.; Carter, C.; Calame, K.; Bond, M.; Hood, L.; Wall, R. Cell 20, 303-312, 1980
A;Title: Two mRNAs with different 3' ends encode membrane-bound and secreted A;Reference number: A37517; MUID:80222873; PMID:6771019
A;Contents: MOPC 104E
                                                F;339-307/Domain:
F;346-417/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-435,'GKPTLYNVSLIMSDTGGTCY' <KAW>
C;Comment: The sequence of residues 1-409 was assumed to be identical with the correspon
C;Comment: During differentiation, B lymphocytes switch from expression of membrane-boun
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Ig mu chain - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S25705
R;Patri, S.; Nau, F.
                                                                           A;Cross-references: EMBL:X59994; NID:gl269; PIDN:CAA42611.1; C;Superfamily: immunoglobulin C region; immunoglobulin C;Keywords: immunoglobulin C;Keywords: immunoglobulin F;483-554/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                  R:Patri, S.; Nau, F.

Mol. Immunol. 29, 829-836, 1992

A;Title: Isolation and sequence of a cDNA c
A;Reference number: S25705; MUID:92342148;
A;Accession: S25705
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S25705
                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-592 < PAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                            EVNAEEEGFENLWTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPVLD--SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PNEVHKHPPAVYLLPPAREQLNLRESATVTCLVKGFSPADISVQWLQRGQLLPQEKYVTS
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         Conservative
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                         22.7%;
                                          10.9%;
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; Pred. No. 6.4e-15;
83; Mismatches 188;
Score 371.5; Ub .,
bred. No. 1.5e-14;
         96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKL
                                                                                                                                                                                                                        ; PMID:1635560
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                                                                                                                                 PID:g1270
                                            592;
         181;
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Query Match 10.8%; Score 370; DB 2; Length 548; Best Local Similarity 24.2%; Pred. No. 1.6e-14; Matches 157; Conservative 108; Mismatches 217; Indels 166; Gaps 31; Matches 157; Conservative 108; Mismatches 217; Indels 166; Gaps 31; Oy 30 LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLN 77	ined D:g41 ion; molog	n C region - mouse (fragment) musculus (house mouse) 1995 #sequence_revision 06-Jan-1995 #text_change 24-May-2001 8864 ker, W.; Schlaak, M.	Qy 600 NVFSCSVMHEALHNHYTOKSLSLSPG 625	Qy 544 LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 599	QY 486 TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG-QPREPQVYTLPPSRDELT-KNQVS 543 : : : : :	374 -IFLIKSAKLSCLVTNLASYD-GLNISWSHQNGKALETHTYFERHLNDTFSARGEA	346FQXVASSCDATPPSPIGVFTIPPSFAD	Db 318 AYSVLTITEREWLSQSAYTCQVEHNKET 345 Qy 369 QCLLSDSGQVLLESNIKVLPTWSTPVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKFKD 428	SLSWFRDGKRIVS VMRATQLQKNLTC	255 DLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALBAKTGKL	Qy 201 VLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITF 254	Qy 165GKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIV 200	Db 115ARSAGAYFLADVDIWGRGLLVTVSSESESHPKVFPLVSCVSSPSDENTVALG 166	63 MPEWLÓGVEKGÓNTYYNPALKŚRĹŚIARDTSKSQVSLŚLSSSKAIDTAVYYC	61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEE	QY 6 PFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
N1 C	A;Note: the sequence was determined from the germline gene R;Goldberg, G.I.; Vanin, E.F.; Zrolka, A.M.; Blattner, F.R. Gene 15, 33-42, 1981 A;Title: Sequence of the gene for the constant region of the mu chain of Balb/c mouse im A;Reference number: A26239; MUID:82051295; PMID:6795090 A;Accession: A26239 A;Molecule type: DNA A;Residues: 1-455 <gol> A;Note: the sequence was determined from the germline gene R;Auffray, C.; Rougeon, F.</gol>	B02039 T. of mouse immunoglobulin mu 6590; PMID:6255422	MHMS Ig mu chain C region, secreted form - mouse C;Species: Mus musculus (house mouse) C;Date: 31-Oct-1980 #sequence revision 31-Oct-1980 #text change 16-Aug-1996	499 NGŚNRGFFIFŚRLEVAKTLWTORKOFTCOVIHEALOKPRKLE	Db 441 RSAPEVYVFPPPEEE-SEDKRTLTCLIQNFFPEDISVQMLGDGKLISNSQHSTTTP-LKS 498 Oy 580 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN-HYTQKSLSLS 623	Qy 522 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 579	462 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ	Qy 414 LGGPSVFLFPFKPXDTLMISRTPEVTCVVVDV-SHEDPEVKFN	QY 355 EKPVWVLNPEAGMWQCLLSDSGQV-LLESNIKVLPTWSTPVEPKSCDKTHTCPPCEAPEL 413	Db 231EVSSVEIFPPKKDVLTRSTIQLYCFIYGHILNDVSVSWLMDDREITDTLA 281	199 TVTCNVAHPASSTKVDKKIVPRDCGCKPCIVP	Db 167SGVHTFPAVLQSDLYTLSSSVTVPSSTWPSE 198 QY 244 RASSSKSWITFDLKNKEYSVKRYTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEA 303	QY 189 NQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGEL	137 QSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQ	70 ISRDNAKNTLYLQMSSLKSEDTAMYYCARQGVSTMIRFAYM	OV 78 -DRADSRRSLWDOGNFPLIIKNLKIEDSDTYICEVEDOKEEVOLLVFGLTANSDTHLLOG 136

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F;129-201/Domain: immunoglobulin homology <IMM2>
F;239-307/Domain: immunoglobulin homology <IMM3>
F;346-417/Domain: immunoglobulin homology <IMM4>
F;346-417/Domain: immunoglobulin homology <IMM4>
F;346-4517/Domain: immunoglobulin homology <IMM4>
F;436-455/Domain: carboxyl-terminal <CTS>
F;14/Disulfide bonds: interchain (to light chain) #status predicted
F;14/Disulfide bonds: #status experimental
F;46,211,243,281,442/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;46,211,243,281,442/Binding site: carbohydrate (Asn) (sovalent) #status experimental
F;136-199,246-305,353-415/Disulfide bonds: #status predicted
F;236,454/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted
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A;Title: Complete amino acid sequence of a mouse mu chain: homology among heavy chain A;Reference number: A02039; MUID:83075344; PMID:6816276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-225,'N',227-257,'S',259-367,'K',369-455 <AUF>
R;Kehry, M.; Sibley, C.; Fuhrman, J.; Schliling, J.; Hood, L.E.
Proc. Natl. Acad. Sci. U.S.A. 76, 2932-2936, 1979
A;Reference number: A26241; MUID:79223904; PMID:111247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into licing perfamily: immunoglobulin C region; immunoglobulin homology C; Ruperfamily: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobus; 21,21,21,00main; immunoglobulin homology < IMM1>
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C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 1-77,'N',79-100,'Q',102-225,'N',227-257,'T',259-367,'K',369-455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A
A; Contents: MOPC 104E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 ESPPGSSPSVQCRSP-RGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVL
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                                                  PPVLD--SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                       STCAASPSTDIL----TFTIPPSFAD-IFLSKSANLTCLVSNLATYE-TLNISWASQSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OSFPNVFPLVSCESPLSDKNLVAMGCLARDFLPSTISFTWN--
APMPEPGAPGFYFTHSILTVTEEEWNSGETYTCVVGHEALPHLVTERTVDKSTG
                                                                                                       PNEVHKHPPAVYLLPPAREQLNLRESATVTCLVKGFSPADISVQWLQRGQLLPQEKYVTS
                                                                                                                                                      PRE----PQVYTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTT 573
                                                                                                                                                                                                                          EPLETKIKIMESHPNGTFSAKGVASVCVEDWNNRKEFVCTVTHRDLPSPQKKFISK----
                                                                                                                                                                                                                                                                            EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 521
                                                                                                                                                                                                                                                                                                                                                                                            THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                       KGSTPQTYKVISTLTISEIDWLNLNVYTCRVDHRGLTFLK---------NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----PEA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NPNVNVFVPPRDGFSGPAPRKSKLICEATNFTPKPITVSWLKDGKLVESGFTTDPVTIEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HQEVNLVV-----MRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLN 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSQVLLSPKSILEGSDEYLVCKIHYGGKNRDLHVPIP------AVAEM 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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22.8%;
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Pred. No. 2.9e-14;
10; Mismatches 180; Indels 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---GMWQCLLSDSGQVLLESNIKVLPTWSTPVEPKSCDK 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKL 308
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Nucleic Acids Res. 14, 2381-2389, 1986
A;Title: Allotypic differences in murine mu-genes.
A;Reference number: A24976; MUID:86176735; PMID:3083402
A;Accession: A24976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig mu chain C region (allele b) - mouse C;Species: Mus musculus (house mouse) C;Decies: Mus musculus (house mouse) C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 21-Jan-2000 C;Accession: A24976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Note: the authors translated the codon AAG for residue 65 as C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: immunoglobulin
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Best Local (
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                                                                                                                                                                                                                                        SSTCAASPSTDIL----TFTIPPSFAD-IFLSKSANLTCLVSNLATYE-TLNISWASQSG
                                                                                                                                                                                                                                                                                THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VKRYTQDPKLQM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVS 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QSFPNVFPLVSCESPLSDKNLVAMGCLARDFLPSTISFTWN----------
APMPEPGAPGFYFTHSILTVTEEEWNSGETYTCVVGHEALPHLVTERTVDKSTG
                                       PPVLD--SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                            PNEVHKHPPAVYLLPPAREQLNLRESATVTCLVKGFSPADISVQWLQRGQLLPQEKYVTS
                                                                                                              PRE----POVYTLPPSRDELT-KNOVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTT
                                                                                                                                                           EPLETKIKIMESHPNGTFSAKGVASVCVEDWNNRKEFVCTVTHRDLPSPQKKFISK----
                                                                                                                                                                                                 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 521
                                                                                                                                                                                                                                                                                                                     KGSTPQTYKVISTLTISEIDWLNLNVYTCRVDHRGLTFLK------NV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSQVLLSPKSILEGSDEYLVCKIHYGGKNKDLHVPIP------AVAEM 110
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                                                                                                                                                                                                                                                                                                                                                           -----GMWQCLLSDSGQVLLESNIKVLPTWSTPVEPKSCDK 401
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; Pred. No. 2.9e-14;
80; Mismatches 180
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C;Accession: A02144
R;Liu, F.T.; Albrandt, K.; Sutcliffe, J.G.; Katz, D.H.
Proc. Natl. Acad. Sci. U.S.A. 79, 7852-7856, 1982
A;Title: Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain cDNA.
A;Reference number: A02144; MUID:83117774; PMID:6818553

A; Accession: A02144

Ig epsilon chain C region (version 1) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_

_change

16-Jul-1999

RESULT

57

450

390

218

432

624

373 566 313 510 253

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A; Molecule type: mRNA
A; Residues: 1-388 LIU>
A; Residues: 1-388 CIUO
A; Croses-references: GB: J00476; NID:g194875; PIDN: AAA38085.1; PID:g387220
A; Croses-references: GB: J00476; NID:g194875; PIDN: AAA38085.1; PID:g387220
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;1-44/Domain: immunoglobulin homology <IM2>
F;81-149/Domain: immunoglobulin homology <IM2>

                                                                                                                                                                                                                                            Ig heavy chain - human (Species: Homo sapiens (man) (Species: Homo sapiens (man) (C;Species: Homo sapiens (man) (C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999 (C;Accession: S15590 R.Neale, G.A.M.; Kitchingman, G.R. Nucleic Acids Res. 19, 2427-2433, 1991 A;Title: mRNA transcripts initiating within the human immunoglobulin mu heavy (A;Reference number: S15590; MUID:91252286; PMID:1904154 A;Accession: S15590
                                                                          A;Cross-references: EMBL:X58529
A;NOTe: the authors translated the codon CAA for residue 265 as Glu G;Superfamily: immunoglobulin Cregion; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;344-415/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-474 <NEA>
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S15590
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F;290-361/Domain: immunoglobulin homology <IM4>
F;10,51,62,133,205,228,332,382/Binding site: carbohydrate (Asn) (covalent)
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Matches 86; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALPAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVSWLMDDREITDTLAQT----VLIKEEGK----LASTCSKLNITEQQWMSESTFTCKVTSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PVNITEP----IQLYCFIYGHILNDV
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    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.6%; Score 363.5; DB 1; 28.2%; Pred. No. 2.5e-14; tive 76; Mismatches 149;
                   10.5%;
    65;
Score 360; DB 2;
Pred. No. 5.3e-14;
5; Mismatches 121
    121;
                                       Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
  Indels
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  50;
  Gaps
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  11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 6
C;Superfamily: immunoglobulin C region; immunoglobulin C;Keywords: immunoglobulin
C;Keywords: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-343 <PAR>
A;Cross-references: EMBL:X68312; NID:g56461; PIDN:CAA48392.1; PID:g818025
                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: spleen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S25644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: S25644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Parker, K.; Bugeon, L.; Soulillou, submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: S25644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig mu chain C region - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1995 #sequence_revision 30-Jan-1998 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ś
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                                       609
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  308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  332
                                                                                                                                                                                                                                                                                                                                                                                                                                                              323 QKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLES
                                                                                                                                                                                                                                                                                                                                    78 DWLNIAVFTCRVDHRGLTFWKNVSSTCAASPSTDILAFP----IPPSFAD-IFLTKSAKL
                                                                                                                                                                                                                                                                                                                                                                                                                           19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                NIKVLPTWSTPVEPKSC----DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPTTYKVTSTLTIKESD-----
  EALPHMVTERTVDKSTG
                                     EALHNHYTOKSLSLSPG
                                                                                                                                                                                                         KCKVSNKALPAPIEKTISKAKGQPRE-----PQVYTLPPSRDEL-TKNQVSLTCLVKGFY 552
                                                                                                                                                                                                                                                   SCLVTNLATYD-TLNISWSSKSGEPLETNTKIMESHPNGTFSAVGVASVCMEDWDNRKEF
                                                                                                                                                                                                                                                                                            TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
                                                                                                                                                                                                                                                                                                                                                                                                                       KSRLICEATNESPKQITVSWLQDGKPVKSGFTTBPVTV-EAKGSRPQTYKVISTLTITES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEKYVTSAPMPEPQAPGRYFAHSILTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKQTISRPKGVALHRPDVYLLPPAREQLNLRESATITCLVTGFSPADVFVQWMQRGQPLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVTISWTRQNGQAVKTHTNISESHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STPVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLE-SNIKVLPTW
                                                                                   PADI FVQWLQRGQPLSSDKYVTSAPMPEPGAPGLYFTHS ILTVTEEEWNSGETYTCVVGH
                                                                                                                        PSDIAVEWESNGQP--ENNYKTTPPVLD--SDGSFFLYSKLTVDKSRWQQGNVFSCSVMH 608
                                                                                                                                                                    VCTVTHRDLPSPQKKFISK----PNEVAKHPPAVYLLPPAREQLILRESATVTCLVKGFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----TEGEVSADEEGFENLWAT 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLQLDETCAEAQDGELDGLWTT 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENNYKTTPPVLD--SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IEKTISKAKGQP-REPQVYTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DTAIR-----VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.5%;
                                         625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 359.5; DB 2
Pred. No. 3.7e-14;
5; Mismatches 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 September 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -WL---SQSMFTCRVDHRGLTFQQNASSMCVPDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132;
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Indels Length 343;

25;

Gaps

77

498 132

191

307

247

homology

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R;McGuire, K.L.; Duncan, W.R.; Tucker, P.W.
Nucleic Acids Res. 13, 5611-5628, 1985
N;Title: Phylogenetic conservation of immunoglobulin heavy chains:
A;Reference number: A02168; MUID:85297761; PMID:2994005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Haire, R.N.; Shamblott, M.J.; Amemiya, C.T.; Litman, G.W. Nucleic Acids Res. 17, 1776, 1989
A;Title: A second Xenopus immunoglobulin heavy chain constant A;Reference number: S03186
A;Accession: S03186
A;Introns: 105/3; 218/3; 324/3
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate int
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                 A,Residues: 1-454 <MCG>
A,Note: the sequence was determined from A,Note: the authors translated the codon C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                       AHEM
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A;Note: the authors translated the codon TT for residue 9 as S.
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain C region - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change
C;Accession: S03186
                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                   C;Accession: A02168
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                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                            g mu chain C region - golden hamster
;Species: Mesocricetus auratus (golden hamster)
;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Aug-1996
                                                                                                                                                                                            ;Accession: A02168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291 YAGSGNLT-LALEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQLRILKGMWNKGTQ-YSCIVTHTSSNTTTIANISQC-TEQCHDNLQVYPLTPTFHD-LY 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNIKVLP-TWSTPVEPKSCDKTHT------CPPCPAPELLGGPSVFLFPPKPKDTLM 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MVTLTCFVTGFNPKEIFIQWMQGGVSISEDKFINTVPMKSDGEQTYFIYSKLAIPAAKWN 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SALIATHODMINGKEAKCKASNKYTÞVEIBKLISKY-KGÖLEBÖNALTÞESKDETIKNÖ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AISRAQHENINATLDLLCIINNFYHGQIKVKWLVNGKQDVSAEASVPTPSKTEDGTYSSS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGDVFTCVVGHEALPLYITQQSIDKSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -VSLTCLVKGFYPSDIAVEWESNG---QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SILSVCAEDWESGDKFSCTVRSQDLPSPVKKTIFKQNEGTPKAPDVYLLPPSAQELIQQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISRTPEVTCVV------VDVSHEDPEV-KFNWYVDGVEVHNAKTKPREEQYNSTYRVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YTLSSQLTILASEWKNSTYKCK---VVHNYTNTKQEKSLKVLPCMAPHVQLFLQSPCMSD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.5%; Score 359.5; DB 2; 28.4%; Pred. No. 5.2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----EPVWVLN-----PEAGMWQCLLSDSGQVLLE
                                                                                                         GGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 625
                                                                                                         germline gene for residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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A;Residues: 2-428 < UED>
A;Cross-references: GB.JO0222; NID:g184755
A;Cross-references: GB.JO0222; NID:g184755
R;Zhang, K.; Saxon, A.; Max, E.E.
J. Exp. Med. 176, 233-243, 1992
J. Title: Two unusual forms of human immunoglobulin E encoded A;Title: Two unusual forms of human immunoglobulin E encoded A;Reference number: PHI214; MUID:92308839; PMID:1613458
A;Accession: PHI214
                                                                                                                                                                                                                                          A;Cross-references: GB:L00022; GB:J000227; GB:V00555; NID:g185035
R;Ueda, S.; Nakai, S.; Nishida, Y.; Hisajima, H.; Honjo, T.
EMBO J. 1, 1539-1544, 1982
A;Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon
A;Reference number: A23195; MUID:84207910; PMID:6327276
                                                                                                                                                                                                                                                                                                                                                                                                                               EMBO J. 1, 655-660, 1982
A;Title: The sequence of a human immunoglobulin epsilon
* pafarance number: A22771; MUID:84236029; PMID:6234164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig epsilon chain C region - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 31-Mar-1981 #sequence revision 13-Jun-1983 #text_change 16-Jul-1999 C;Accession: A22771; A23195; PH1214; A93491; A90824; A94418; B93933; S02438; R;Flanagan, J.G.; Rabbitts, T.H. R;Flanagan, J.G.; Rabbitts, T.H. EMBO J. 1, 655-660, 1982
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F;238-306/Domain: immunoglobulin homology <IMM3>
F;335-416/Domain: immunoglobulin homology <IMM4>
F;345-416/Domain: immunoglobulin homology <IMM4>
F;45,112,139,192,210,238,257,280,326,441/Binding site: carbol F;135-198,245-304,352-414/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: A22771;
A;Accession: A22771
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A; Residues: 1-428 < FLA>
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A; Molecule type:
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; Pred. No. 5.3e-14;
84; Mismatches 171;
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A;Notecuse type: mRNA
A;Residues: 382-391 <HE2>
A;Rolecule type: mRNA
A;Residues: 382-391 <HE2>
A;Cross-references: GB:S55276; NID:g263168; PIDN:AAB24858.1; PID:g263169
A;Cross-references: B cell myeloma U-266
A;Note: sequence extracted from NCBI backbone (NCBIP:125299)
A;Accession: A46536
A;Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
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A, Molecule type: mRNA
A, Residues: 382-426 <HEL>
A, Residues: 382-426 <HEL>
A, Cross-references: GB:S55273; NID:g263166; PIDN:AAB24857.1; PID:g263167
A, Cross-references: B cell myeloma U-266
A, Experimental source: B cell myeloma U-266
A:Note: sequence_extracted from NCBI backbone (NCBIP:125297)
A:Note: sequence_extracted from NCBI backbone (NCBIP:125297)
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A; Residues: 'GAWTL', 6', X', 8-16,'B', 18-43,'B', 45-52,55-92,95-97,'B',99-121,'B',123,'L',12
A; Experimental source: myeloma protein Nd
R; Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.; G
Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982
A; Title: Cloning and sequence determination of the gene for the human immunoglobulin eps
A; Reference number: A93933; MUID:83065234; PMID:6815656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eur. J. Immunol. 23, 159-167, 1993
A;Title: Characterization of four novel epsilon chain mRNA and A;Reference number: A46536; MUID:93122085; PMID:8419166
A;Accession: C46536
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A;Residues: 320-428 <ZH2>
A;Residues: 320-428 <ZH2>
A;Residues: 320-428 <ZH2>
A;Residues: 320-428 <ZH2>
A;Rote: sequence extracted from NCBI backbone (NCBIN:141701, NCBIP:141702)
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A;Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces A;Reference number: A53116; MUID:94103254; PMID:8276835
A;Accession: A53116
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A; Residues: 98-352 < IKES
R; Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon,
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A; Residues: 1-358, 'L', 360-428 < MAX>
A; Residues: 1-358, 'L', 360-428 < MAX>
A; Cross-references: GB: J00222; NID: g184755
A; Note: this sequence difference may be due to polymorphism
A; Note: this sequence difference may be due to polymorphism
A; Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.R; Bennich, H.R; H.R; Bennich,
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A;Residues: 320-428 <ZHA>
A;Crose-references: EMBL:X63693; GB:S38668; NID:g32987
A;Crose-references: EMBL:X63693; GB:S38668; NID:g32987
R;Seno, M.; Kurokawa, T.; Ono, Y.; Onda, H.; Sasada, R.; Igarashi, K.; Kikuchi, M.; S
Nucleic Acids Res. 11, 719-726, 1983
Nucleic Acids Res. 11, 719-726, 1983
A;Title: Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon
A;Reference number: A93491; MUID:83168897; PMID:6300763
A;Accession: A93491
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A;Residues: 1-40;68-114;427-428 <KEN>
A;Cross-references: GB:L00022; NID:g185035
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A;Accession: A94418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; not compared with conceptual translation
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FEBS Lett. 224,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: preliminary
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hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate (Superfamily: immunoglobulin C region; immunoglobulin homology C; Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immu F; 22-87/Domain: immunoglobulin homology <IM1> F; 128-195/Domain: immunoglobulin homology <IM2> F; 232-301/Domain: immunoglobulin homology <IM3> F; 338-407/Domain: immunoglobulin homology <IM3> F; 338-407/Domain: immunoglobulin homology <IM4> F; 14/Disulfide bonds: interchain (to light chain) #status predicted F; 15-105, 29-85, 135-193, 239-299, 345-405/Disulfide bonds: #status predicted F; 21, 49, 99, 1.46, 252, 275/Binding site: carbohydrate (Asn) (covalent) #status experi F; 121, 209/Disulfide bonds: interchain (to heavy chain) #status predicted S 밁 S 밁 á 밁 8 밁 S 밁 á 밁 S 밁 δ A;Map position: 14q32.33-14q32.33
A;Introns: 1/1; 104/1; 211/1; 319/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap A;Residues: 401-428 <HE3>
A;Cross-references: GB.S53497; NID:g263162; PIDN:AAB24855.1;
A;Experimental source: B cell myeloma U-266
A;Note: sequence extracted from NCBI backbone (NCBIP:123483)
C;Genetics: A; Cross-references: A;Gene: GDB:IGHE Matches 119; Query Match Best Local Similarity 347 548 493 400 407 292 232 433 174 118 362 267 63 AVHEAASPSQTVQRAVSVNPG VMHEALHNHYT-QKSLSLSPG IEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRT-----LACL ---HQEVNLVVMRATQLQKNLTCEV-WGPTSPKLMLSLKLENKEAKVSKRE---KPVWVL 361 TODPKL----QMGKKLPLHLT-------LPQALPQYAGSGNL---TLALEAKTGKL IQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICR VKGFYPSDIAVEWESN--GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL----PPSRDELTKNQVSLTCL RKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGTRDW SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW TQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKC-ADSNPRGVSAYLSRPSPFD-LFI QSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVD----LSTASTTQEGELAS SGHYATISLLTVSGAWAKQMFTCRVAHTPSSTDW-----VDNKTFSVCSRDFTPPTVKIL TOSPSVFPLTRCCKNIPSNATSVTLGCLATGYFPEPVMVTWDTGSLNGTTMTLPATTLTL Conservative GDB:119335; OMIM:147180 -----DKTHTC------PPCPAPELLGGPSVFLFPPKPKDTLMI PEAGMWQCLLS------DSGQVLLESNIKVLPTWSTPVEPKSC-10.5%; 69; Score 359; DB 1; Pred. No. 5.3e-14; 427 625 Mismatches 155; DB 1; Length 428; Indels PID:g263163 heterotetramer; immunoglobu 98; #status experimental 406 809 492 173 399 346 547 291 231 432 62 18 into

IgM heavy chain

constan

A;Residues: 1-453 <HAR> A; Molecule type: mRNA

A; Cross-references: EMBL: X67301; NID: g38407; PIDN: CAA47714.1; PID: 938408

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A;Experimental source: cell line Ab 63
C;Genetics:
A;Map position: 14q32
A;Map position: immunoglobulin C region; immunoglobulin homology
C;Superfamily: immunoglobulin C region; immunoglobulin
C;Keywords: glycoprotein; heterotetramer; immunoglobulin
F;21-90/Domain: immunoglobulin homology <IMM1>
F;21-90/Domain: immunoglobulin homology <IMM2>
F;227-305/Domain: immunoglobulin homology <IMM3>
F;247-199/Domain: immunoglobulin homology <IMM3>
F;244-415/Domain: immunoglobulin homology <IMM3>
F;244-415/Domain: immunoglobulin homology <IMM3>
F;14/Disulfide bonds: interchain (to light chain) #status predicted
F;28-88,134-197,244-303,351-413/Disulfide bonds: #sratus predicted
F;46,209,272,79,400/Binding site: Carbohydrate (Asn) (covalent) #status predicted
F;214,452/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted
F;291/Disulfide bonds: interchain (to mu chain in another subunit)
                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-438, 'GKPTLYNVSLIMSDTASTCY' <BER>
A;Residues: 1-438, 'GKPTLYNVSLIMSDTASTCY' <BER>
A;Residues: 1-438, 'GKPTLYNVSLIMSDTASTCY' <BER>
A;Residues: 1-438, 'GKPTLYNVSLIMSDTASTCY' <BER>
A;Residues: An immunoglobulin heterotetramer subunit consists of two identical light (kap c);Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la c;Superfamily: immunoglobulin cregion; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin homology <IMMIL
F;21-92/Domain: immunoglobuli
F;439-479/Domain: carboxyl-terminal <CTS>
F;14/Disulfide bonds: interchain (to light chain)
F;28-90,137-200,249-308,356-418/Disulfide bonds:
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A; Residues: 439-479 <BE2>
A; Accession: A02164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig mu chain C region, membrane-bound form - rabbit C;Species: OryCtclagus cuniculus (domestic rabbit) C;Date: 04-Dec-1986 #sequence_revision 30-Jun-1991 #text_change C;Accession: A02165; A02164
R;Bernstein, K.E.; Alexander, C.B.; Reddy, E.P.; Mage, R.G. J. Immunol. 132, 490-495, 1984
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                                                                                                                              F;130-202/Domain: immunoglobulin homology <IMM2>
F;242-310/Domain: immunoglobulin homology <IMM3>
F;349-420/Domain: immunoglobulin homology <IMM4>
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         #status
                                                   #status
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C;Species: Gallus ga
C;Date: 07-Sep-1990
C;Accession: S00390
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S00390
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A; Residues: 1-504 < PAR>
                                                                                                                                                                                                                                                                                                        A;Title: Chicken immunoglobulin gamma-heavy chains: limited A;Reference number: S00390; MUID:88283642; PMID:3135182 A;Accession: S00390
                                                                                                                                                                                                                                                                                                                                                                  R;Parvari, R.; Avivi, A.; Lentner, F.; Ziv, EMBO J. 7, 739-744, 1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig gamma chain (clone 36) - chicken (fragment)
N;Alternate names: Ig nu chain
                                                                                                                                                                                          ;Superfamily: immunoglobulin C region; immunoglobulin;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                             Species: Gallus gallus (chicken)
[Bate: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jan-2000]
                                                                                                                 Matches
                                                                                                                                   Query Match
Best Local
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                                                                                                                                   Similarity
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                                       VAAISSTGSGTNYG-SAVKGRATISRDN-GQSTLRLQLNNLRAEDTGTYYCARDLGYGDL
                                                           IKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYIC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VAKHPPAVYVLPPAREQLVLRESATVTCLVKGFSPADVFVQWQQRGQPLSSDKYVTSAPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FPL----AFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LD--SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QPRE-POVYTLPPSRDELT-KNOVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GKALDTHMNITESHPNATFSAMGEASVCAEDWESGEQFTCTVTHADLPFPLKHTISKSRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STTPSP----GIQVFPIAPSFADT-FLSKSARLICLVTDLTTYG-SLNISW-----ASHN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSGNLTLALEAK-TGKLHQEVNLVVMRATQ-----LQKNLTCEVWGPTSPKLMLSLKLE 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEEEGFENLWTT
---EVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG 166
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                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.5%; Score 358.5; DB 1 24.6%; Pred. No. 6.5e-14;
                                                                                                                                 10.5%;
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                                                                                                                   89;
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                                                                                                                                   Score 358; DB 2;
Pred. No. 7.5e-14;
                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    E.; Tel-Or, S.;
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                                                                                                                                                   Length 504;
                                                                                                                                                                                                              homology
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                                                                                                                   Indels 186;
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C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 23-Jul-1999
C;Cate: 29-May-1998 #sequence_revision 29-May-1998 #text_change 23-Jul-1999
C;Cate: 29-May-1998 #sequence_revision 29-May-1998 #text_change 23-Jul-1999
C;Cate: 29-May-1998 #sequence 29-May-1998 #text_change 23-Jul-1999
C;Cate: 29-May-1998 #sequence_revision 29-May-1998 #text_change 23-Jul-1999
C;Cate: 29-May-1998 
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160082
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C; Superfamily:
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C; Genetics:
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A; Residues: 1-71 < RES>
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63
                                                   13
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                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLLSPSSAGGISWEGSG-----
                                                   ILGNOGSFLTK 71
                                                                                                                                                      MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLAFTVEKLTGSGELWWQAERASSSKSWITF----DLKNKEVSVKRVTQDPKLQMGKKL
   ILGNQGSFLTK 71
                                                                                                            MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTVFACMAVHEALPMRFSQRTLQKQAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QDWLSGERFTCTVQHEELPLPLSKSVYRNTGPTTPPLIYPFAPHPEELSLSRVTLSCLVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR--EEQYNSTYRVVSVLTVLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EV-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----VPPVAPEVO-----VLHASSCTPSQSESVELL-------CLVTGFSPASA 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQKNLTCEVWG--PTSP 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KTLSVSQ---LELQDSGTWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YAGQIDAWGHGTEVIV---SSASPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISLDAKLRCLVVNLP-SDSSLSVTWTRE--KSGNLRPDPMVLQEHFNGTYSASSAVPVST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human (fragment)
                                                                                                                                                                                                                                                                                                                                        T-cell surface glycoprotein CD4; immunoglobulin homology
                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  GB:S79267; NID:g1086922; PIDN:AAB35273.1; PID:g1086923
                                                                                                                                                                                                                                                   10.5%;
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                                                                                                                                                                                                                              <u>.</u>
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                                                                                                                                                                                                                        Score 357; DB 2;
Pred. No. 6.9e-15;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      503
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                                                                                                                                                                                                                                                                                 Length 71
                                                                                                                                                                                                                              Indels
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RESULT

67

C.; Barnikol, H.U.; Hilschmann,

z

#text_change 16-Jul-1999

protein BOT.

Peculiar amino-acid

MHHUBT

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Ig epsilon chain C region - rat (Species: Rattus norvegicus (Norway rat))
C;Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 16-Jul-1999
C;Accession: A93442; A90937; A02143
R;Hellman, L.; Pettersson, U.; Engstrom, A.; Karlsson, T.; Bennich, H.
Nucleic Acids Res. 10, 6041-6049, 1982
A;Title: Structure and evolution of the heavy chain from rat immunoglobulin A;Reference number: A93442; MUID:83064537; PMID:6292865
A;Accession: A93442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IQA and IGM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin C;Keywords: immunoglobulin homology <IMI>
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F;223-291/Domain: immunoglobulin homology <IM3>
F;223-291/Domain: immunoglobulin homology <IM4>
F;327-398/Domain: immunoglobulin homology <IM4>
F;46,99,170,240,265,369,419/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 'N', 169-307, 'L', 309-342 < KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: A cloned cDNA probe for rat immunoglobulin epsilon heavy A;Reference number: A90937; MUID:83182019; PMID:6820340 A;Contents: myeloma IR162 A;Contents: myeloma IR162 A;Accession: A90937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Experimental source: strain LOU/c/Wsl, immunocytoma R;Kindsvogel, W.R.; Reddy, E.P.; Moore, J.M.; Faust J DNA 1, 335-343, 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-429 < HEL>
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Best Local (
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nes 101; Conserv
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623
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                                                                                                                                                                                                                                               -NITVTWVRERKKSIGSASQRSTKHHNATTSITSILPVDAKDWIEGEGYQCRVDHPHFPK
SPG 625
                                                                                            ENNYKTTPPVLDSDGS---FFLYSKLTVDKSRWQQGNVFSCSVMHEALHN-HYTQKSLSL 622
                                                                                                                                                                         PIEKTISKAKGQPREPQVYT-LPPSRDELTKNQVSLTCLVKGFYPSDIAVEW--ESNGQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGM--------
                                                KSQHSTTP-
                                                                                                                                                PIVRSITKAPGKRSAPEVYVFLPPEEEE--KDKRTLTCLIQNFFPEDISVQWLQDSKLIP
                                                                                                                                                                                                                                                                         FTCKVTSQGENYWAHTRRCSDDE-PRGVITYLIPPSPLD-LYENGTPKLTCLVLDLESEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KNFTCHV--THAPSTFVS-----DLTIRARPVNITKPTVDLLHSSCDPNAFHSTIOL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.4%; Score 355.5; DB 1; Length llarity 27.8%; Pred. No. 8.5e-14; Conservative 69; Mismatches 114; Indels
                                              -LKYNGSNQRFF1FSRLEVTKALWTQTKQFTCRV1HEALREPRKLERT1SK
                                                                                                                                                                                                                                                                                                                                                                                            -----PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
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A;Reference number: A02163; N
A;Accession: A02163
A;Molecule type: protein
A;Residues: 1-391 <BAR>
C;Comment: This protein has n
C;Genetics:
                                                                                                                                  A;Introns: 103/1; 209/1; 317/1 C;Superfamily: immunoglobulin F;336-405/Domain: immunoglobul
                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-426 <RES>
A;Cross-references: GB:M15398; NID:g176797; PIDN:AAA35416.1; PID:g176798
                                                                                                                                                                                                                                                                                 R;Sakoyama, Y.; Hong, K.
Proc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987
A;Title: Nucleotide sequences of immunoglobulin ep
A;Reference number: 136948; MUID:87147196; PMID:3
A;Accession: 136948
                                                                                                                                                                                                                                                                                                                                                                            C;Species: Pan troglodytes (chimpanzee)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change
C;Accession: I36948
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F;65-137/Domain: immunoglobulin homology <IMM1>
F:175-243/Domain: immunoglobulin homology <IMM2>
F:175-243/Domain: immunoglobulin homology <IMM3>
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Superfamily: duplication; glycoprotein; heterotetramer; immunoglobulin; transmembrane
C;Reywords: duplication; glycoprotein; heterotetramer; immunoglobulin; transmembrane
F;1-41/Domain; pre-C <VAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: GDB:IGHM
A;Cross-references:
                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;147,210,217,378/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                          Genetics:
                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            332 GPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNIKVL--PT 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84;
                                                                           h 10.3%;
Similarity 28.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 10.4%; Score 353.5; DB 1; Similarity 27.8%; Pred. No. 9.9e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -ENNYKTTPPVLD--SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLKQTISRPKGVALHRPDVYLLPPAREQLNLRESATITCLVTGFSPADVFVQWMQRGQPL
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in: immunoglobulin
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                                                            Conservative
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                                                                                                                                C region; immunoglobulin lin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OMIM: 147020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    region
                                                                           Score 353; DB 2;
Pred. No. 1.2e-13;
                                                        Mismatches 144; Indels 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -WL---GQSMFTCRVDHRG-LTFQQNASSMCGPD
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                                                                                             DB 2; Length 426;
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A;Gene: GDB:IGHM
A;Cross-references: GDB:120086; OMIM:147020
A;Cross-references: GDB:120086; OMIM:147020
A;Map position: 14q32.33-14q32.33
A;Map position: 105/1; 217/1; 323/1; 433/1; 471/3
A;Introns: 1/1; 105/1; 217/1; 323/1; 433/1; 471/3
C;Complex: An immunoglobulin heterotetramer subunit consists of C;Complex: An immunoglobulin heterotetramer subunit disulfide
                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-39, L', 41-432, 'GKPTLYNVSLVMSDTAGTCY'
A; Cross-references: EMBL:X14940
R; Rabbitts, T.H.; Forster, A.; Milstein, C.P.
Nucleic Acids Res. 9, 4509-4524, 1981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 29-Jan-1993 #sequence_revision 23-Aug-1997 #text_change 22-Jun-1999
C;Accession: S16510; S09357; S16656; B26243; A02167
R;Dorai, H.; Gillies, S.D.
Nucleic Acids Res. 17, 6412, 1989
A;Title: The complete nucleotide sequence of a human immunoglobulin genomic A;Reference number: S09357; MUID:89366690; PMID:2505237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, A;Reference number: S16656 A;Accession: S16656
                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 433-436,'N',438,'E',440-447,'T',449-473 <RAB>
A;Cross-references: GB:K01310; NID:g184715; PIDN:AAB59422.1;
C;Comment: During differentiation, B lymphocytes switch from
                                                                                                                                                                                                                                                                                                                            A;Title: Human immunoglobulin heavy chain genes: evolutionary comparisons A;Reference number: A26243; MUID:82059479; PMID:6795593 A;Accession: B26243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-432,'GKPTLYNVSLVMSDTAGTCY'
A;Cross-references: EMBL:X14940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X14939
A;Note: the authors translated the codon AAC for A;Note: the sequence of residues 1-432 was assume A;Accession: 809357
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                                                                                                                                                                                    C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Note: the authors translated the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 433-473 <DOR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S16510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKQEKQR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEVTRAEWEQKDEFICRAVHEAASPSQTVQRTVSVNPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---LSTASATQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGGTFEDSTKKC-ADSNPR 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IKVLPTWSTPVEPKSC---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEAKVSKRE--KPVWVLN-----PEAGMWQCLLS-----DSGQVLLESN 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGSLNGTTMTLPATTLTPSGHYATISLLTVSGAWAKQMFTCRVAHTPSSTDW-----VDN
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two identical light linked pentamers.

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Ig mu chain C region, screening (domestic rabbit, C;Species: Oryctolagus cuniculus (domestic rabbit, C;Species: Oryctolagus cuniculus (domestic rabbit, C;Bate: 13-Aug-1986 #text_change C;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change C;Accession: A02164
C;Accession: A02164
R;Bernstein, K.E.; Alexander, C.B.; Reddy, E.P.; Mage, R.G.
J. Immunol. 132, 490-495, 1994
J. Immunol. 132, 490-495, 1994
J. Immunol. 132, 490-495, 1994
                                                                                                         F;130-202/Domain: immunoglobulin homology <IMM2>
F;342-310/Domain: immunoglobulin homology <IMM3>
F;349-420/Domain: immunoglobulin homology <IMM3>
F;349-420/Domain: immunoglobulin homology <IMM4>
F;14/Disulfide bonds: interchain (to light chain) #status predicted
F;28-90,137-200,249-308,356-418/Disulfide bonds: #status predicted
F;28-90,137-200,249-308,56-418/Disulfide bonds: #status predicted
F;46,114,212,261,277,284,445/Binding site: carbohydrate (Asn) (covalent) #s
F;219,457/Disulfide bonds: interchain (to mu chain in another subunit) #status
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F;237-305/Domain: immunoglobulin homology <IMM3>
F;234-415/Domain: immunoglobulin homology <IMM4>
F;33-473/Domain: immunoglobulin homology <IMM4>
F;433-473/Domain: immunoglobulin homology <IMM4>
F;433-473/Domain: carboxyl-terminal #status predicted <CTS>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;28-88,134-197,244-303,351-413/Disulfide bonds: #status experimental
F;46,209,272,779/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;214/Disulfide bonds: interchain (to heavy chain) #status experimental
F;214/Disulfide bonds: interchain (to mu chain in another subunit) #status experim
                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-458 «BER»
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin pomology F; 21-92/Domain: immunoglobulin homology 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Complete sequence of a cloned cDNA encoding rabbit A;Reference number: A02164; MUID:84088930; PMID:6418803 A;Contents: a2 allotype A;Accession: A02164
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        Query Match
Best Local Similarity
Matches 116; Conserv
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          10.2%;
ilarity 24.6%;
Conservative 8
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0
          Score 349; DB 1;
Pred. No. 2.3e-13;
0; Mismatches 167;
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                                                           Length 458;
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          108;
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          Gaps
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                                                                                                                                                                 predict
                                                                                                                                                                                                                                                                                                                A.Cross references EMBL:X14940
R;Harindranath, N.; Donadel, G.; Sigounas,
Mol. Immunol. 30, 111-112, 1993
A;Title: Comparison of complete nucleotide A;Reference number: S37767; MUID:93109369; A;Accession: S37767
A; Molecule type: DNA
A; Residues: 1-17;105-186;200-259;296-322;339-416,'D',418-452
A; Cross-references: GB: K01310; NID: g184715
                                                                                R;Rabbitts, T.H.; Forster, A.; Milstein, C.P.
Nucleic Acids Res. 9, 4509-4524, 1981
A;Title: Human immunoglobulin heavy chain genes: evolutionary
A;Reference number: A26243; MUID:82059479; PMID:6795593
A;Accession: A26243
                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-190,'8',192-414,'V',415-452 < HAR>
A; Cross-references: EMBL:X67292; NID:g38405; PIDN:CAA47708.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, A;Reference number: S16656 A;Accession: S16656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 29-Jul-1981 #sequence revision
C;Accession: S09357; S16656; S37767; A2
R;Dorai, H.; Gillies, S.D.
Nucleic Acids Res. 17, 6412, 1989
A;Title: The complete nucleotide sequen
                                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-39,'L',41-452
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A; Residues: 1-452 < DOR1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STTPSP----GIQVFPIAPSFADT-FLSKSARLICLVTDLTTYG-SLNISW-----ASHN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LD--SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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A26243; A26244; I37749; I37750; A02162;
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IgM heavy chain constan

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Nucleic Acide Res. 8, 1993-5991, 1980

A;Title: Cloning of human immunoglobulin mu gene and comparison with mouse mu A;Reference number: I37748; MUID:81124312; PMID:6450943

A;Accession: I37749
                                                                                                                                                                                     F;14/Disulfide bonds: interchain (to light chain) #status experimental F;28-88,134-197,244-303,351-413/Disulfide bonds: #status experimental F;46,209,272,279,439/Binding site: carbohydrate (Asn) (covalent) #status experimental F;214,451/Disulfide bonds: interchain (to heavy chain) #status experimental F;214,051/Disulfide bonds: interchain (to mu chain in another subunit) #status experiment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GDB:120086; OMIM:147020
A;Map position: 14932.33-14932.33
A;Introns: 1/1; 105/1; 217/1; 33/1; 433/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. The IgM subunits associate into disulfide linked pentamers.
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; glycoprotein; heterotetramer; immunoglobulin C;21.90/Domain: immunoglobulin homology <IMM1>
F;21.90/Domain: immunoglobulin homology <IMM1>
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Science 182, 287-291, 1973
A;Title: Complete amino acid sequence of the mu heavy chain of a human IgM immunoglobuli
A;Reference number: A02088; MUID:74005511; PMID:4742735
A;Rontents: annotation; Waldenstrom's macroglobulin Ou, sequence, disulfide bonds, and c
A;Note: this sequence differs from that shown at a number of positions; this sequence had c;Comment: During differentiation, B lymphocytes switch from expression of membrane-boun
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A;Molecule type: protein
A;Rosidues: 100-144,'E',146-162,'E',164,'E',166-214,'G',216-262,'D',264-295,'D',297-414,
A;Rosidues: 11 four combinations of the 191-Ser/Gly and 215-Val/Gly polymorphisms have beer
A;Note: all four combinations of the 191-Ser/Gly and 215-Val/Gly polymorphisms have beer
R;Watanabe, S.; Barnikol, H.U.; Horn, J.; Bertram, J.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 354, 1505-1509, 1973
A;Title: The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal), 1
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A;Tittle: Cloning and partial nucleotide sequence of human immunoglobulin mu chain cDNA
A;Reference number: A26244; MUID:81077306; PMID:6777778
A;Accession: A26244
                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;127-199/Domain: immunoglobulin homology <IMM2>F;237-305/Domain: immunoglobulin homology <IMM3>F;344-415/Domain: immunoglobulin homology <IMM4>F;3432-452/Domain: carboxyl-terminal <CTS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Note: this sequence has been revised in reference A02162
R;Putnam, F.W.; Florent, G.; Paul, C.; Shinoda, T.; Shimizu,
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A;Residues: 1-17,'BPS',22,'T',24-82,'N',84-90,'Z',92-93,'B',95,'B',97-144,'E',146-162,'
A;Accession: B02162
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A;Residues: 433-452 <TAK2>
A;Residues: 433-452 <TAK2>
A;Residues: 433-452 <TAK2>
A;Cross-references: EMBL:V00563; NID:g33454; PIDN:CAA23826.1; PID:g825684
A;Cross-references: EMBL:V00563; NID:g33454; PIDN:CAA23826.1; PID:g825684
A;Cross-references: EMBL:V00563; NID:g33454; PIDN:CAA23826.1; PID:g825684
A;Mihaesco, E.; Barnikol-Watanabe, S.; Barnikol, H.U.; Mihaesco, C.; Hilschmann, N. Eur. J. Blochem. 111, 275-286, 1980
Eur. J. Blochem. 111, 275-286, 1980
A;Tille: The primary structure of the constant part of mu-chain-disease protein BOT.
A;Tille: The primary structure of the constant part of mu-chain-disease protein BOT.
A;Reference number: A02162; MUID:81066716; PMID:6777162
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A;Residues: 347-370 <TAK1>
A;Cross-references: EMBL:V00562; NID:g33448; PIDN:CAA23825.1; PID:g929649
A;Accession: I37750
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A;Molecule type: mRNA
A;ReBidueB: 298-386;436-452 <DOL>
A;ReBidueB: 298-386;436-452 <DOL>
A;Cross-referenceB: GB:J00257; NID:g185053; PIDN:AAA53508.1; PID:g185056; GB:J00258;
A;Cross-referenceB: GB:J00257; NID:g185053; PIDN:AAA53508.1; PID:g185056; GB:J00258;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: GDB:IGHM
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                                                   Local Similarity
          Conservative
                                              10.2%;
     62;
Score 348; DB 1; Length 452;
Pred. No. 2.5e-13;
2; Mismatches 110; Indels
     46;
                                                                                                                                                                                                    #status experimental
Gaps
     11;
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          280 SHPNSTFTAKGHASVCREEWESGEKFTCTVQHSDLPSPLKQSLSRPKDVANDPPSVFVLP 339
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90 80	332 GPTSPKLMLSIKLENKEAKVSKREKPVWVLNPEAMMQCLLSDSGQVLLE-SNIKVLPTW 390 : : : : : : : : : : : : : : : : :
B 8	391 STPVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 450 : ::::::: : :::::::: : ::::::
B &	451 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 510
β δ	511 IEKTISKAKGQP-REPQVYTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP 566 ::: :
P 64	567 ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 624
Ş	625 G 625
Db	433 G 433
RESULT 73 S03961 If mu chair C;Species: C;Date: 28 C;Accessior R;Ishiguro, FEBS Lett. A;Title: Nu A;Reference A;Accessior A;Molecule A;Recessior A;Reference A;Accessior A;Reference A;Accessior A;Molecule A;Reference A;Reference A;Reference A;Reference A;Reference A;Reference A;Reference A;Reference A;Reference A;Cross-Femily	RESULT 73 \$03961 Ig mu chain C region - house shrew (fragment) C;Species: Suncus murinus (house shrew) C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000 C;Accession: \$03961 C;Accession: \$1 Ichihara, Y.; Namikawa, T.; Nagatsu, T.; Kurosawa, Y. FEBS Lett. 247, 317-322, 1989 A;Title: Nucleotide sequence of Suncus murinus immunoglobulin mu gene and comparison wit A;Reference number: \$03961; MUID:89232144; PMID:2497033 A;Accession: \$03961 A;Rolecule type: DNA A;Residues: 1-457 <15H> A;Rolecule type: DNA A;Residues: 11-457 <15H> A;Canerferice: EMBL:X13920 C;Genetics: Mullin C region: immunoglobulin homology C;Genetics: immunoglobulin C region: immunoglobulin homology
Query Match Best Local S Matches 109	Match 10.2%; Score 348; DB 2; Length 457; Local Similarity 23.7%; Pred. No. 2.6e-13; les 109; Conservative 90; Mismatches 160; Indels 100; Gaps 18;
β δ	204 FOKASSIVYKKEGEQVEFSPPLAFTVEKLTGSGELWWQAER-ASSSKSWITFDLKN 258 :
B 8	259 KEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVV 316
B &	317 MRATQLQKNLTCEVW
8 8	353 KREKPVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVEPKSCDKTHTCPPCPAPE 412
Ş	413 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 472
9 8	473 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE-PQVYTLP 531

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Ig epsilon chain C region (version 2) - mouse C;Species: Mus musculus (house mouse) C;Date: 30-Jun-1987 #text_change C;Date: 30-Jun-1987 #text_change C;Accession: A02145 R;Ishida, N.; Ueda, S.; Hayashida, H.; Miyata, T.; Honjo, T. EMBO J. 1, 1117-1123, 1982 A;Title: The nucleotide sequence of the mouse immunoglobulin eps: A;Reference number: A90966; MUID:84236092; PMID:6329728 A;Accession: A02145
RESULT
IS0731
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C;Speci
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F;220-288/Domain: immunoglobulin homology <IMM3>
F;220-288/Domain: immunoglobulin homology <IMM3>
F;325-396/Domain: immunoglobulin homology <IMM4>
F;23-75,122-181,227-286,332-394/Disulfide bonds: #status
F;43,84,167,239,262,417/Binding site: carbohydrate (Asn)
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A; Residues: 1-423 <ISH>
A; Note: the sequence was
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A; Introns: 91/1; 199/1;
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   g heavy chain - nurse s
Species: Ginglymostoma
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Best Local Similarity
Matches 115; Conserv
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                                                                                                                                                                                                                                                        DSDGS---FFLYSKLTVDKSRWQQGNVFSCSVMHEALHN-HYTQKSLSLSPG
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                                                                                                                                                                                               KSNGSNQGFFIFSRLEVAKTLWTQRKQFTCQVIHEALQKPRKLEKTISTSLG
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27.9%;
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Pred. No. 3.5e-13;
8; Mismatches 131;
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      ehark)
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                          Ig mu chain C region - dog (tentative sequence) C;Species: Canis lupus familiaris (dog) C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1 C;Accession: A93131; A94246; A02169 R;McCumber, L.J.; Capra, J.D.
                                                                                                                                                                                                   MHDG
MHDG
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76

Capra, J.D. 565-570, 19

13-Jul-1981

#text_change

31-Mar-2000

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A;Gene: IgH
C;Superfamily: immunoglobulin C region; immunoglobulin
c:4ca_610/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDB:
A;Molecule type: mRNA
A;Residues: 1-577 <VAZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mol. Immunol. 29, 1157-1158, 1992
A;Title: Nucleotide sequence of a nurse shark immunoglobulin A;Reference number: IS0731; MUID:92357056; PMID:1495502
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Best Local S
Matches 155
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                             DSDG-SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                             NPLEPSVSVLLPTTEELSAQRFLSLTCLVRGFRPREIFVKWTTNDKPVNPSNYKNTEVTA
                                                                                                                                                        NAKTKPREEQYNS---TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK-G
                                                                                                                                                                                                                                                                                                                      TVSSSEEIESRKFAIIVCSISDFHSK----SISVTWLKNGRSVDSGIFTSP-----VCEA
                                                                                                                                                                                                                                                                                                                                                                                     KKGTYTL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGOGLEWIVYYYSSSMNNYAPAIKORFTAAK---DTSNNIFALEMRSVKIDDTAIYYC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GNQG----SFLTKGPSKLNDRADSRRSLWDQGN--FPLIIKNLKIEDSDTYICEV
ESDNTSFFLYSLLSIAAEEWASGASYSCVVGHEAIPLKIINRTVDKSSG
                                                                                           OPREPOVYTLPPSRDELTKNO-VSLTCLVKGFYPSDIAVEWESNGOPEN--NYKTTPPVL
                                                                                                                                                                                          ------GYTAKILPP-PVEQVLLEATVTLTCV---VSNLHSGVNFTWLQD-----
                                                                                                                                                                                                                       CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
                                                                                                                                                                                                                                                     NGNFSVTSRLRVPYAEWFDRAVYTC----QVKYK---EVIQSWNITGPQVSECH----
                                                                                                                                                                                                                                                                                       NKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWS-TPVEPKSCDKTHT
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                                                                                                                                                                                                                                                                                                                                                                                                                 LTGSGELWWQAERASSSKSWITFDLKNKEVS--VKRVTQDPKLQMGKKLPLHLTLPQALP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----TRRMSGYEYLGGHSGYWGQGTMVTVTTATP--SSPTLY------GLVSSC
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                                                                                                                          -EKTLKSEIAHDSGEHSDGAISKLDISTEAWLSEVVFECVVNHQYLPTPLRDSIHKERIE
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); Mismatches
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hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate in (Superfamily: immunoglobulin C region; immunoglobulin homology C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;20-89/Domain: immunoglobulin homology <IMM1> F;126-196/Domain: immunoglobulin homology <IMM1> F;126-196/Domain: immunoglobulin homology <IMM2> F;234-302/Domain: immunoglobulin homology <IMM3> F;341-412/Domain: immunoglobulin homology <IMM4> F;341-412/Domain: immunoglobulin homology <IMM4> F;430-450/Domain: interchain (to light chain) #status predicted F;17-87,133-194,241-300,348-410/Disulfide bonds: #status predicted F;27-87,133-194,241-300,348-410/Disulfide bonds: hstatus predicted F;211,449/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted F;288/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted
R;Schwager, J.; Mikoryak, C.A.; Steiner, L.A.
Proc. Natl. Acad. Sci. U.S.A. 85, 2245-2249, 1988
A;Title: Amino acid sequence of heavy chain from Xenopus
A;Reference number: A94192; MUID:88176921; PMID:2451244
A;Accession: C31933
                                                                                                                                                Ig mu chain C region - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Mar-1990 #sequence_revision 30-Jun-1992 #text_change 20-Sep-1999
C;Accession: C31933
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A;Title: Amino acid sequence of the Fc region of a canine immunoglobulin M: interspecies A;Reference number: A94246; MUID:78180587; PMID:653360
A;Contents: Moo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-177 < MCC>
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A;Residues: 178-450 <WAS>
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                            ERSVDKSTGKPTLYNVSLVLSDTAGZ 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                OKSLSLSPG-----LQLDETCAE 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VQKGQPVPPDSYVTSAPMPEPQAPGLYFAHSILTVSEEEWNAGETYTCVVAHESLPNRVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NASSMCTSDQPV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----CEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLES 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPVMLTLPPEVSGFIPPRDAFFGBPRKSQLICQASGFSPRQVWSL--RDGKQIESGVTTN
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                                                             laevis IgM deduced from
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C;Accession: B35503

R;Gilmore, G.L.; Bard, J.A.; Birshtein, B.K.
J. Immunol. 141, 1754-1761, 1988
A;Title: DNA rearrangements affecting both variable and A;Reference number: A30503; MUID:88315788; PMID:2842402
A;Accession: B30503
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A;Residues: 1-453 <SCH>
C;Superfamily: immunoglobulin C region;
C;Keywords: immunoglobulin
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A;Experimental source: myeloma
A;Note: the authors translated
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C;Species: N
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A; Residues: 1-112 <GIL>
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;Species: Mus musculus (house mouse)
;Date: 31-Mar_1989 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                              ;1-70/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   342 LKLENKEAKVSKREKPV--------WVLNPEAGMWQCLL--SDSGQVLL 380
                                                                 61
                                                                                                                                                                                                                                                                               ly: immunoglobulin C region; immunoglobulin immunoglobulin
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                                                                                                                               SLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDW
                                                                                            LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY 552
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                              PSDIAVEWESNG
                                                                 MSGKEFKCKVNNKDLPAPIERTISKPKGE-
                                                                                                                                                                SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW 492
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                                                                                                                                                                                               Score 331.5;
Pred. No. 4e-1
17; Mismatches
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4e-13;
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RiGreenberg, A.S.; Avila, D.; Hughes, M.; Hughes, A.; McKinney, Nature 374, 168-173, 1995
A;Title: A new antigen receptor gene family that undergoes rearr A;Reference number: $60266; MUID:95183140; PMID:7877689
A;Accession: $60266
A;Status: preliminary; nucleic acid sequence not shown
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S60266
RESULT 80
$31436
$31436
Ig upsilon chain - axolotl (fragment)
C;Species: Ambystoma mexicanum (axolotl)
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A;Residues: 1-684 <GRE>
A;Cross-references: EMBL:U18701; NID:g699442; PIDN:AAB48195.1; PID:g699443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  novel antigen receptor precursor - nurse shark C;Species: Ginglymostoma cirratum (nurse shark) C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change C;Accession: $60266
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                                                                                                                                               SLSLSPGLQLDET 631
                                                                                                                                                                                                                                                                                                                                                               PE-VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP
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                                                                                                                                                                                   LDSGYRTQVDSEKGSGSSFVTDRLRLTAAEWNSDTTYSCLVGHPSLNRDLIRSTNKSNGK
                                                                                                                                                                                                                     PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH-----NHYTQK
                                                                                                                                                                                                                                                       TPVKASIRKANVSOMHPPKVYLLHPSTDEIDTENSATLMCLATNFHPAEIYVGWMANDTL
                                                                                                                                                                                                                                                                                         APIEKTISKAK-GOPREPOVYTLPPSRDEL-TKNOVSLTCLVKGFYPSDIAVEWESNGO-
                                                                                                                                                                                                                                                                                                                               LENIKVFWQVNGVERKKGVETQNPEWSGSKSTIVSKLKVMASEWDSGTEYVCLVEDSELP
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                                                                                                             PSSVNVSVVLSDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.7%; Score 330.5; DB 2
llarity 23.5%; Pred. No. 4.7e-12;
Conservative 83; Mismatches 237
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T-ceil surface glycoprotein CD4 (allele 1) - pig (fragment) (;Species: Sus scrofa domestica (domestic pig) (;Date: 20-Feb-1995 #sequence_revision 19-Apr-1996 #text_change C;Accession: I47131; S21461 R;Gustafsson, K.; Germana, S.; Sundt, T.M.

J. Immunol. 151, 1365-1370, 1993 A;Title: Extensive allelic polymorphism in the CDR2-like region A;Reference number: I47131, MUID:93329116; PMID:8335933 A;Accession: I47131
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                                                                                                          A;Cross-references: EMBL:X65629; NID:g1928; PIDN:CAA46583.1; PID:g388232 C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology C;Keywords: g1ycoprotein; T-cell
                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-99 < GU2>
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C;Superfamily: immunoglobulin C region; immunoglobulin
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A; Residues: 1-433 < FEL>
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A;Reference number: S31436
A;Accession: S31436
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                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VSV-----KRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GEPVEVSWKAGSTT----MPGGKTFPAAQQQATALSTSSQIRIPAYEWGTNSYSCSVKHKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKS-----WIT----FDLKNKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YFSYSMLTIQKSDWDKRETFTCVAAHSAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---DGQGTFSTTSQINVTKSDWASGDKYTCKVEHPATSSRAEDTIHNCADSQTPY---QP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSTEIHKTITSAECKKATSKPSVQV-----LQSSCADTDGNGSI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQYIDSDGTFTAMSYLNITKNEWERGDEFTCKVKHFDLFFPLSRSVSKPTGRSFAPTMYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLLSDSGQVLLESNIKVLPT-WST-----PVEPKSCDKTHTCPPCPAPELLGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQ
                                                                                         immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.2%; Score 313.5; DB 2
23.6%; Pred. No. 2.6e-11;
                     8.9%; Score 305.5; DB 60.2%; Pred. No. 1.2e-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -ELVCLISGYTPDNIQVRWLVNDKMAPIQGQTSP-----PQK----
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                611
                                            DB 2;
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                                          Length
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Conservative

16;

Indels

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Gaps

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A;Cross-references: GB:X00353; NID:g1575; PIDN:CAA25100.1; PID:g1576
C;Comment: This immunoglobulin belongs to the JgA-g subclass. It was isolated from a r C;Comment: An immunoglobulin belongs to the JgA-g subclass. It was isolated from a r C;Complex: An immunoglobulin beterotetramer subunit consists of two identical light (k hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin; plasma F;86-152/Domain: immunoglobulin homology <IM1>
F;86-152/Domain: immunoglobulin homology <IM2>
F;38,286/Binding site: carbohydrate (Asn) (covalent) #status predicted
A; Molecule type: DNA
A; Residues: 1-357 <BUR>
C; Superfamily: immunoglo
C; Keywords: immunoglobu
                                                                                                                        R;Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K.L. EMBO J. 8, 4041-4047, 1989
A;Title: The IgA heavy-chain gene family in rabbit: clos A;Reference number: S09264; MUID:90076124; PMID:2512120
                                                                                                                                                                                                      Ig alpha chain C region - rabbit (fragment)
(;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
C;Accession: S09269
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A;Title: Genes encoding alpha-heavy chains of rabbit IgA: characterization of A;Reference number: A02174; MUID:84144059; PMID:6322114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AHRB
Ig alpha chain C region - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985
C;Accession: A02174
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A; Residues: 1-299 < KNI>
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                                                                                 A; Status: not compared with
                                                                                                       A; Accession: S09269
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                     Superfamily: immunoglobulin C
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 8.9%; Score 305; DB 1;
Similarity 31.6%; Pred. No. 5.2e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSLTCLVKGFYPSDIAVEWESNGQ---PENNY----KTTPPVLDSDGSFFLYSKLTVDKSRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLPSSAETWKARTEFTCTVTHPEIDSGSLTATISRGVVTP--PQVHLLPPPSEELALNEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDLGD-LLLGRDASLTCTLSGLKNPEDAV-FTW--EPTNGNEPVQQRAQRDLSGCYSVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QCLGQKSAACHVEYNSVI--NESLPVPFPDCCPANSCCTCPSSSSRNLISGCQPSLSLQR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QCLLSDSGQVLLESNIKVLPTWSTPVEPKSCDKTHTCPPCPAP---ELLGG--PSVFLFP
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                                                                                 conceptual translation
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                     region;
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                     immunoglobulin
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                     homology
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                                                                                                                                           sequence analysis
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Ig mu chain
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A;Molecule type: DNA
A;Residues: 1-338 «BUR»
A;Residues: immunoglobulin C region; immunogi
C;Keywords: immunoglobulin
F;228-300/Domain: immunoglobulin homology «IMM»
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EMBO J. 8, 4041-4047, 1989
A;Title: The IgA heavy-chain gene family in rabbit: cloning
A;Reference number: S09264; MUID:90076124; PMID:2512120
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
C;Accession: S09276
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNG--QPENNY---KTTPPVLDSDGSFFLY 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YPCGCYSVSSVLPGCAEPWNAGTEFTCTVTHPEIEGGPLTAKISKDTGAIIPPQVHLLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEAGMWQCLLS---DSGQ-VLLESNIKVLPTWSTPVEPKSCDKTHTCP-PCPAPELLGGP 417
  NOGDTYSCMVGHEGLAEHFTORTIDRLAG
                                            QQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                         VTLTCLVRGFSPKDVLVSWRHQGQEVPEDSFLVWKSMPESSQDKATYAITSLLRVPAEDW
                                                                                                                                    VSLTCLVKGFYPSDIAVEWESNGQ--PENNY---KTTPPVLDSDGSFFLYSKLTVDKSRW
                                                                                                                                                                              VLPSSAETWKARTEFTCTVTHPEIDSGSLTATISRGVVTP--PQVHLLPPPSEELALNEQ
                                                                                                                                                                                                                              VLTVLHQDWLNGKEYKCKVSNKALPA-PIEKTISKAKGQPREPQVYTLPPSRDELTKN-Q 541
                                                                                                                                                                                                                                                                           PDLGD-LLLGRDASLTCTLSGLKNPEDAV-FTW--EPTNGNEPVQQRAQRDLSGCYSVSS
                                                                                                                                                                                                                                                                                                                       PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
                                                                                                                                                                                                                                                                                                                                                                  QCLGQKSAACHVEYNSVI--NESLPVPFPDCCPANSCCTCPSSSSRNLISGCQPSLSLQR 116
                                                                                                                                                                                                                                                                                                                                                                                                               QCLLSDSGQVLLESNIKVLPTWSTPVEPKSCDKTHTCPPCPAP---ELLGG--PSVFLFP 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLIRVPAEDWNONESYTCVVGHEGLAEHFTORTIDRLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----TYRVVSVLTVLHQDWLNGKEYKCKVSNKALP-APIEKTISKAKGQPREPQVYTLPP 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLSLQRPFLRD-LLLNSNASLTCTLRGLKNPEGAV-FTW-----EPTNG-NKPVQQSVQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEENSVACHVEHNYDKGQHVTVPS----PPECQPPTPGPSDTT-TCPCPCPSPS-CGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 302; DB 2;
Pred. No. 9.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 338,
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of 13

85

a

region

(clone 12022)

horn

shark (fragment)

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Ig alpha chain C region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47175
R;Brown, W.R.; Butler, J.E.
Mol. Immunol. 31, 633-642, 1994
A;Title: Characterization of a C alpha gene of swine.
A;Reference number: I47175; MUID:94254897; PMID:7545929
A;Accession: I47175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 86
I47175
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A;NOte: the sequence was determined from the differentiated gene
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;1-438/Domain: C region <CRE>
F;20-87/Domain: immunoglobulin homology <IM1>
F;20-87/Domain: immunoglobulin homology <IM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Heterodontus francisci (horn shark)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999
C;Accession: S00980
R;Kokubu, F:; Hinds, K.; Litman, R.; Shamblott, M.J.; Litman, G.W.
EMBO J. 7, 1979-1988, 1988
A;Title: Complete structure and organization of immunoglobulin heavy chain constant reginary capacity and constant reginary capacity capacity and constant reginary capacity ca
A;Cross-references:
C;Genetics:
A;Gene: IgACalpha
                                                                                                                                              A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-342 <BRO>
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F;228-291/Domain: immunoglobulin homology <IM3>
F;330-400/Domain: immunoglobulin homology <IM4>
F;366,200,245,275,374,411,415,425/Binding site: carbohydrate (Asn)
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A; Residues: 1-438 < KOK>
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                                                                                             EMBL:U12594; NID:g555826; PIDN:AAA65943.1; PID:g555827
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    RESULT
A46507
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RESULT 87
S09270
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A;Title: The IgA heavy-chain gene family in rabbit: cloning A;Reference number: S09264; MUID:90076124; PMID:2512120
A;Accession: S09270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993
C;Accession: S09270
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A; Residues: 1-348 <BUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;133-199/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig alpha chain C region - rabbit (fragment)
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Matches
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Best Local
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305
                                                                                                                                                   185
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                                                                                                                                                                                                                                                                                                                                                                                   84;
                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                           -LLLGSDASLTCTLRGLKYPEDAV-FTWEPTNGNEF--VQQSPQRDPC-GCYSVSSVLPG
                                   VFSCSVMHEALHNHYTQKSLSLSPG 625
                                                                                                             CLVKGFYPSDIAVEWESNG--QPENNY---KTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
                                                                                                                                                   CAEPWNAGTEFTCTVTHPEIEGGSLTATISKDTGSLTPPQVHLLPPPSEELALNALVTLT
                                                                                                                                                                                     LHQDWLNGKEYKCKVSNKALP-APIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLT
                                                                                                                                                                                                                                                                                                                                             QCLLSDSGQVLLESNIKVLPTWSTPVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSVMHEALHNHYTQKSLSLSPG----LQLDETCAEAQ 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DPWNKGETFSCTAAHSELKSALTATITKPKVNTFRPQVHLLPPPSEELALNELVTLTCLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLLGSNASLTCTLSGLKKSE-GVSFTWQPSGGK-DAVQASPTRDSC-GCYSVSSILPGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSKSSQSV---NVPCKVLPS-----DP-----CPQCCK-----PSLSLQPPALAD-
SYTCVVGHEGLAEHFTORTIDREAG
                                                                                                                                                                                                                                                               TLMISRTPEVTCVVVDVSHEDPEVKFNWY-VDGVEVHNAKTKPREEQYNSTYRVVSVLTV
                                                                                                                                                                                                                                                                                                         QCLEYDSAACHVEYNSVINESLPVPF-PDPCEQCH-CPSCEE-----PSLSLQRPDLRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGFSPKDVLVRWLQGGQELPRDKYLVWESLPEPGQAIPTYAVTSVLRVDAEDWKQGDTFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KGFYPSDIAVEWESNGQ--PENNY---KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
                                                                         CLVRGFSPKDVLVYWRKKDVEVPENSFLVWKPLPEPGQDPTTYAVTSLLRVSAEDWNQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEAE
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milarity 31.4%;
Conservative 43
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunoglobulin homology <IMM:
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31.7%;
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; Pred. No. 2.1e-10;
43; Mismatches 109
                                                                                                                                                                                                                                                                                                                                                                                   41;
                                                                                                                                                                                                                                                                                                                                                                                 Score 295.5; DB 2;
Pred. No. 2.3e-10;
1; Mismatches 119;
329
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of 13

88

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Ig alpha chain C;Species: Gall C;Species: 18-Jun C;Accession: AR;Mansikka, A. J. Immunol. 149
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A;Reference number: A46507; MUID:92340889; P
A;Accession: A46507
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A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:109906, NCI
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Species: Gallus gallus;Date: 18-Jun-1993 #sequ;Accession: A46507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 8.7%; Score 295.5; DB 2; Similarity 24.3%; Pred. No. 4.5e-10; 61; Conservative 87; Mismatches 264;
                                    SPG
                                                                                                                                                                                                                                                                                                                                                                                  KLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNIKVL-PTWSTPVEPKSCDK
                                                                                                                                                                                                            GVSVSWSRSSGGGLDV----SQTEDRQADGRYTVRSFLRVCAEEWNGGETFGCSVREEGV
                                                                                                                                                                                                                                                                                                                                                                                                                        CLVEGLPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSL 342
                                                                    PISPQNYLIFGP--EKDGDFYSLYSKLKVSVEDWQRGDVFGCVVGHDGIPLNFIHKSIDK
                                                                                                     P--ENNYKTTPPVLDSDGSFF-LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
                                                                                                                                       -VVAEESIRKETDTPLHAPSVYVFPPPAEELSLQETATLTCMASSFLPSSILLTWTQQNQ
                                                                                                                                                                      PAPIEKTISKAKGOP-REPOVYTLPPSRDELT-KNOVSLTCLVKGFYPSDIAVEWESNGO
                                                                                                                                                                                                                                          EVKFNWYVD----GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL
                                                                                                                                                                                                                                                                             THGALKEPVTATVSTDCDATPQL----QVSLLPPTLEE-LLVSHNATVTCVVSNAAAAD-
                                                                                                                                                                                                                                                                                                                                                -LQDNEEMTPAPE-----SDESGCSDC--TESG-VTQWSRVNVTRKSWEGGAQ-FGCRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LQGN-EFVCRAQHAATGA-----DVKETIGGDGVCPIFTSKVTLLSDPTQEDFERRVLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTGSGELWWQAERASSSKSWITFDLKNK-----EVSVKRVT--QDPKLQMGKKLPLHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFLPPPVTVTWTTGGAADATAV------TSLPVATTGGTYSLTTALTVPREQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SQLELQDSGTWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEK 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --ASGCGACAGSIDAWGHGTEVIVSSASASRPTLYQLLPLPSDCPDP---NVTIG-CLVT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSV-----QCRSPRGKNIQGGKTLSV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGIDDDGSGTGYGPAVQGRATISRDN--GQSTVRLQLNNLRAEDTATYYCAKG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KILGNOGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLLLAALPGLMAAVTLDESGGGLQTPGGALSLVCKASGFTFSSYSMGWMRQAPGKGLEWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLLVLQLALLPAATQGNKVVLGKK--GDTVELTCTAS--QKKSIQFHW-----KNSNQI 59
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                                    625
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                                                                                                                                                                                                                                                                                                             -TCPPCPA-PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP
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Ig mu chain C region, memorane-pound (controlled) (form shark) (c;Species: Heterodontus francisci (horn shark) (c;Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text_change 16-C;Accession: S01854; C32716; Ā46530 R;Kokubu, F:; Hinds, K.; Litman, R.; Shamblott, M.J.; Litman, G.W. EMBO J. 7, 1979-1988, 1988 A;Title: Complete structure and organization of immunoglobulin heal A;Reference number: S00980; MUID:88328985; PMID:3138109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;438-458/Domain: Liaus | F;27-85,130-188,235-289,337-398/Disulfide bonds: #scattorydrate (Asn) F;164,200,245,275,374,411,415,437/Binding site: carbohydrate (Asn)
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F;228-291/Domain: immunoglobulin homology <IMM3>
F;228-291/Domain: immunoglobulin homology <IMM3>
F;330-400/Domain: immunoglobulin homology <IMM4>
F;330-400/Domain: immunoglobulin homology <IMM4>
F;438-458/Jomain: transmembrane #status predicted <TMM>
F;27-85,130-188,235-289,337-398/Disulfide bonds: #status predicted
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A; Residues: 1-99 < KO2>
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A;Cross-references: EMBL:X07781
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Best Local :
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  AEEWASGASYSCVVGHEAI
                                             KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGELDGLWTTD 647
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Pred. No. 3.6e-10;
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1987
PLKIINRTVNKSSDSS-DHIWIED
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A;Introns: 100/1; 206/1; 309/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin cregion; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglo F;1-438/Domain: C region <CRE>
F;20-87/Domain: immunoglobulin homology <IM1>
                                                                              F;123-190/Domain: immunoglobulin homology <IM2>
F;228-291/Domain: immunoglobulin homology <IM3>
F;330-400/Domain: immunoglobulin homology <IM4>
F;164,200,245,275,374,411,415,425/Binding site:
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A; Residues: 1-438 < KOK>
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A; Residues: 1-357 <BUR>
C; Superfamily: immunoglobulin C region; immunoglobulin C; Keywords: immunoglobulin
C; Keywords: immunoglobulin homology <IMM>
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Ig alpha chain C region - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
C;Accession: S09265
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Best Local Similarity
Matches 89; Conserv
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  Query Match
Best Local Similarity
Matches 117; Conserv
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    Conservative
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8.6%; Score 293.5; DB 1
25.8%; Pred. No. 4.1e-10;
Live 68; Mismatches 163
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                                      DB 1;
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
C;Accession: S09274
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   NVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                 GCAEPWNAGTEFTCTVTHPEIEGSSLTATISKDTGSLTPPLVHLLPPPSEELALNALVTL
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                                                                     TCLVRGFSPKDVLVSWTNKGVKVPENSFLVWKPLPEPGQDPTTYAVTSLLRVPAEDWNQN
                                                                                                                                           TCLVKGFYPSDIAVEWESNG--QPENNY---KTTPPVLDSDGSFFLYSKLTVDKSRWQQG
                                                                                                                                                                                                                                                                               VLHQDWLNGKEYKCKVSNKALP-APIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSL
                                                                                                                                                                                                                                                                                                                                                        -LLLGSDASLTCTLRGL--KDPEGAVFTWGPTNGNE--PVQQSPQRDPC-GCYSVSSVLP
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A;Residues: 1-367 <CDHs
A;Cross-references: GB:K00389; NID:g212204; PIDN:AAAA8923.1; PID:g212205
A;Cross-references: GB:K00389; NID:g212204; PIDN:AAAA8923.1; PID:g212205
C;Complex; An immunoglobulin heterotetramer subunit consists of two identical light disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;49-133/Domain: immunoglobulin homology <IMM2>
F;151-219/Domain: immunoglobulin homology <IMM4>
F;151-219/Domain: immunoglobulin homology <IMM4>
F;347-367/Domain: immunoglobulin homology <IMM4>
F;347-367/Domain: carboxyl-terminal <CTS>
F;541-119,303,354/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;126,366/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted
F;126,366/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Mesidues: 1-343 <BUR>
A;Residues: 1-343 <BUR>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;232-305/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                  Ig alpha chain C region - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
C;Accession: S09272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Dahan, A.; Reynaud, C.A.; Weill, J.C.
Nucletc Acids Res. 11, 5381-5389, 1983
A;Title: Nucleotide sequence of the constant region of a A;Reference number: A02170; MUID:83299221; PMID:6310496
A;Accession: A02170.
                                                                                                                                                                               A;Title: The IgA heavy-chain gene family in rabbit: cloning A;Reference number: S09264; MUID:90076124; PMID:2512120 A;Accession: S09272
                                                                                                                                                                                                                                                                       R;Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K.L. EMBO J. 8, 4041-4047, 1989
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S09272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               354 REKP---VWVLN--PEAGMWQCLLSDSGQVLLESNIKVLPT-WSTPV-----EPKSC 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DKTHTC--PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP-EVKFNW 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAPMAENPENESYVAYSVLGVGAEEWGAGNVYTCLVGHEALPLQLAQKSVDRASG 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEKGGKLETALGK-RVLQSNGLYTVDGVATVCASEWDGGDGYVCKVNHPDLLFPMEEKMR 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SKRMECGLEPVVQQDI----AIRVITPSFVD-IFISKSATLTCRVSNMVNADGLEVSW-W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPPVLDS--DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region - chicken (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESYSCVVAHEGLAEHFTORTIDRLAG 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KTKASNARPPSVYVFPPPTEQLNGNQRLSVTCMAQGFNPPHLFVRWMRNGEPLPQSQSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KAK-GQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.5%;
ilarity 30.8%;
Conservative 4
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18; Pred. No. 4.6e-10;
48; Mismatches 126; Indels
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A;Note: this sequence was determined from the differentiated generically: immunoglobulin C region; immunoglobulin homology C;Keywords: glycoprotein; heterotetramer; immunoglobulin; transmer; 1:244/Domain: C region (fragment) < CRE>
F;11-244/Domain: immunoglobulin homology < IMM>
F;111-181/Domain: transmembrane #status predicted < TWM>
F;26,155,192,196/Binding site: carbohydrate (Asn) (covalent) #su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-244 <LIT's
A;Residues: 1-244 <LIT's
A;Cross-references: EMBL:X07785; NID:963965; PIDN:CAA30618.1; PID:963966
A;Note: this sequence was determined from the differentiated gene
R;Kokubu, F.; Hinds, K.; Litman, R.; Shamblott, M.J.; Litman, G.W.
EMBO J. 7, 1979-1988, 1988
A;Title: Complete structure and organization of immunoglobulin heavy chain constant regi
A;Reference number: S00980; MUID:88328985; PMID:3138109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig heavy chain C region (clone 5301) - horn shark (fragment)
C;Species: Heterodontus francisci (horn shark)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 21-Jan-2000
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 21-Jan-2000
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S12328
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A; Residues: 200-244 < KOK>
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Best Local
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nes 81; Conservative
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173
                                                                                                                                       541 QVSLTCLVKGFYPSDIAVEWESNGQPEN--NYKTTPPVLDSD-GSFFLYSKLTVDKSRWQ 597
                                                                                                                                                                                                                                           483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        266 YLVWKPLPEPGQDPTTYAVTSLLRVSAEDWNQGDSYSCVVGHEGLAEHFTQRTIDRQAG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150
                                                                                                                                                                                                                                                                                                                                   428 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY-----NSTYRVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPTNG----NEFVQQSVQSYPCGCYSVSSVLPGCAEPWNAGTEFTCTVTHPEIEGGSLTA 205
                                                                                            FISTICLVRGFSPREIFVKWTVNDKSVNPGNYKNTEVMAENDNSSYFIYSILSIAAEEWA 172
                                                                                                                                                                                                                                      SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQV-YTLPPSRDELTKN 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y---KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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  SGASYSCVVGHEAIPLKIINRTVNKSSDSS-----DHIWIEDNEEESGNIWTT
                                             QGNVFSCSVMHEALH----NHYTQKSLSLSPGLQLDETCAEAQDGELDGLWTT 646
                                                                                                                                                                                           STVDISAQSWLSGVDFYCVVSHQDLPTPLRDFIHKEKNKDLREPSVSVLLPPADDVSAQR
                                                                                                                                                                                                                                                                                      EQVILEATVTLTCV----VSNAPYGVNVSW-----TQEQKPLKSEIAVQPGEDSDSVI
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                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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33.9%; Pr
ative 35;
                                                                                                                                                                                                                                                                                                                                                                                     39; Mismatches
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Pred. No. 8.9e-10;
5; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                           Score 284; DB 2
Pred. No. 7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 244
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A;Cross-references: EMBL:X07782; NID:g63961; PIDN:CAA30615.1; PID:g833623
A;Note: the sequence was determined from the differentiated gene
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical lig
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;1-393/Domain: C region (fragment) <CRE>
F;1-42/Domain: immunoglobulin homology (fragment) <IM1>
F;78-145/Domain: immunoglobulin homology <IM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999 C;Accession: S01852 R;Kokubu, F; Hinds, K.; Litman, R.; Shamblott, M.J.; Litman, G.W. EMBO J. 7, 1979-1988, 1988
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A;Map position: 14q32.33-14q32.33
A;Introns: 1/1 103/1; 210/1
C;Superfamily: immunoglobulin C region; immunoglobulin C;Keywords: immunoglobulin C;Keywords: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-393 < KOK>
                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Complete structure A;Reference number: S00980; A;Accession: S01852
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C;Genetics:
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;Species: Heterodontus francisci (horn shark)
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Best Local Similarity
Matches 100; Conserv
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28.3%; Pred. No. 1.3e-09;
ative 47; Mismatches 137
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C; Superfamily: C; Keywords: gly: F; 3-81/Domain:
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T-cell surface glycoprotein CD4 (allele 2) - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 20-Feb-1995 #sequence_revision 19-Apr-1996 #text_change
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J. Immunol. 151, 1365-1370, 1993
A;Title: Extensive allelic polymorphism in the CDR2-like A;Reference number: 147131, MUID:93329116, PMID:8335933
A;Accession: 147132
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                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X65630; NID:g1929; PIDN:CAA46584.1; PID:g388233 C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology
                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-99 < GU2>
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Best Local S
Matches 55
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;3-81/Domain: immunoglobulin homology <IMM>
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55; Conser
SFPLIIKNLEVTDSGIYICEVEDKRIEVQLLVFRLTAS
                                  NEPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTAN 128
                                                                                           KKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGP-SKLNDRADSRRSLWDQG
                                                                      KAGDLAELPCHSSQKKNLPFSWKNSDQIKILRSHRNLWHKASVTELSSRLDSKKNMWDHG
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                                                                                                                                               Conservative
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                                                                                                                                           Score 280.5; DB 2;
Pred. No. 3.6e-10;
9; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 281.5; DB 1
Pred. No. 1.8e-09;
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S09266
Ig alpha chain C region - rabbit (fragment)
C;Specles: Oryctolagus cuniculus (domestic rabbit)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
C;Accession: S09266
C;Accession: S09266
A;Molecule type: protein
A;Residues: 1-16, Z; 18',B',20,'B',22-34,'Q',36-45,'Z',47-51,'B',53-56,'ZB',59-61,'B',
303,'B',305-346,'Q',348-353 <PUT>
A;Note: this is the final paper in a series
A;Note: amidation states of residues 178, 197, 238, 239, 243, 244, 287, and 318 were t
R;Kratzin, H.; Altevogt, P.; Ruban, E.; Kortt, A.; Staroscik, K.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 356, 1337-1342, 1975
A;Title: The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro.), II: the
A;Reference number: A91662; MUID:76023781; PMID:809331
A;Accession: A91662
A;Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig alpha-1 chain C region - human (Species: Homo sapiens (man) (Species: Homo sapiens (man) (C;Species: Homo sapiens (man) (C;Date: 22-May-1981 #sequence_revision 03-Oct-1995 #text_change 20-Oct-2000 (Accession: A2236; A92249; A91662; S38979; B53110; A02171 (A2360; A92249; A91662; A91662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Putnam, F.W.; Liu, Y.S.V.; Low, T.L.K.

J. Biol. Chem. 254, 2865-2874, 1979
A;Title: Primary structure of a human IgAl immunoglobulin. IV.
A;Reference number: A92249; MUID:79151016; PMID:107164
A;Contents: myeloma protein Bur; disulfide bonds
A;Accession: A92249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Mechanisms of divergence and convergence of the A;Reference number: A94653; MUID:84130179; PMID:6421489 A;Accession: A22360
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A;Title: The IgA heavy-chain gene family in rabbit: cloning A;Reference number: S09264; MUID:90076124; PMID:2512120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-352 <BUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n 8.2%;
Similarity 32.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRTPEVTCVVVDVSHEDPE-VKFNWY-VDGVEVHNAKTKPREEQYN-STYRVVSVLTVLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YSCVVGHEGLAEHFTQRTIDRLAG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESNASLTCTLSGL--KDPEGAVFTWNPTNGNEFVQQST----QSYPCGCYSVSSVLPGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEGQNL----TVLYPECKDPNSDPTPCPCPPITCGEPSLSLQRPDIGD-LLL 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QDWLNGKEYKCKVSNKALP-APIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VRGFSPKDVLVSWTHNGTLVVPKDSFLVWKPLPEPGQEPTTYAVTSLLRVPAEDWNQGDS
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Pred. No. 1.8e-09;
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QQGNVFSCSVMHEALHNHYTQKSLSLSPG-

--LQLDETC 632

305

KKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTC

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306

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VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG--SFFLYSKLTVDKSRW 596 SVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKS-GNTFRPEVHLLPPPSEELALNEL SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-RPALED-LLLGSEANLTCTLTGL-RDASGVTFTWTPSSGK--SAVQGPPERDLCGCYSVS

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PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV 482

186

Matches

Similarity

Conservative

TGKLHQEVNLVVMRATQ--LQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLN 362

132;

Indels

Gape

SGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVP--

PEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVEPKSCDKTHTCPPCPAPELLGGPSVFLF 422

--CPVPSTPPTP----SPSTPPTPSPSCC-HPRLSLH 130

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187 483 131 423 101

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A;Cross-references: GDB:11933; OMIM:146900
A;Map position: 14q32.33-14q32.33
A;Introns: 1/1; 103/1; 223/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapper distribution) immunoglobulin cregion; immunoglobulin homology
C;Complex: An immunoglobulin cregion; immunoglobulin homology
C;Reywords: chromoprotein; duplication; glycoprotein; heterotetramer; immunoglobulin; tre
F;140-206/Domain: immunoglobulin homology <IM1>
F;243-315/Domain: immunoglobulin homology <IM2>
F;26-85,77-101,123-180,147-204,250-313/Disulfide bonds: #status experimental
F;105,111,113,119,121/Binding site: carbohydrate (Ser) (covalent) #status experimental
F;122,182/Disulfide bonds: interchain (to secretory component) (partial) #status experimental
F;192/Disulfide bonds: interchain (partial) #status experimental
F;192/Cross = link: alpha-1-microglobulin-Ig alpha complex chromophore (Cys) (interchain to F;352/Disulfide bonds: interchain (to J chain) (partial) #status experimental
F;352/Disulfide bonds: interchain (partial) #status experimental
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A;Molecule type; protein
A;Molecule type; protein
A;Residues: 188-196, D',198-201 <FAL>
A;Residues: 188-196, D', 198-201 <FAL>
A;Residues: 188-196, D', 198-201 <FAL>
A;Residues: 188-196, D', 198-201 <FAL>
A;Residues: 188-196, D', Gotz, H.; Hilschmann, N.
R;Yang, C.Y.; Kratzin, H.; Gotz, H.; Hilschmann, N.
R;Yang, C.Y.; Kratzin, H.;
R;Yang, C.Y.; Kratzin, N.
A;Reference number: A91684; MUID:80114124; PMID:393607
A;Reference number: A91684; MUID:80114124; PMID:393607
A;Reference number: A91684; MUID:80114124; PMID:393607
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A;Title: Location of a novel type of interpolypeptide chain A;Reference number: A53110; MUID:94103241; PMID:7506257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-16,'Z',18,'B',20,'B',22-34,'Q',36-45,'Z',47-51,'B',53-56,'ZB',59-61,'B','R',232-237,'QQ',240-243,'Q',245-283,'Q',285-289,'E',291-303,'B',305-353 <KRA>
A;Experimental source: myeloma protein Tro
R;Fallgreen-Gebauer, E.; Gebauer, W.; Bastian, A.; Kratzin, H.D.; Eiffert, H.; Zimmerm Biol. Chem. Hoppe-Seyler 374, 1023-1028, 1993
A;Title: The covalent linkage of secretory component to IgA. Structure of sIgA.
A;Reference number: 388978; MUID:94121784; PMID:8292260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Residues: 346-351, 'X', 353 < CAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: GDB: IGHA1
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                                                   Query Match
Best Local :
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                                               8.2%;
; Score 280.5; DB 1; ; Pred. No. 1.8e-09; 49; Mismatches 132;
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SEQUENCE FROM N.A. TISSUE=Pancreas; MEDLINE=22388257; EStrausberg R.L., Fe
                                                                                                                                                                               SEQUENCE FROM N.A., AND VARIANT TRP-26 MEDILINE=91216786; PubMed=1708753; McDougal J.S.; Hodge T.W., Sasso D.R., McDougal J.S.; "Humans with OKT4-epitope deficiency h
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Genome Res.
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Angari-Lari M.A., Muzny D.M., Lu
Malley T., Gibbs R.A.;
"A gene-rich cluster between the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Littman D.R., Maddon P.J., "Corrected CD4 sequence."; Cell 55:541-541(1988).
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don P.J., Axel R.;
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RA Alteschul S.F., Zeebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rahia S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
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RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
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Wu H., Kwong P.D., Hendrickson W
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Tarr G.E., H
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                                                                                                                                                                                                                                                    human CD4.
                                                                                                                                                                                                                                                                                                                                                                                                             Hendrickson W.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang J., Yan Y., Garrett T.P., Liu J.,
Tarr G.E., Husain Y., Reinherz E.L., He
"Atomic structure of a fragment of hum
immunoglobulin-like domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90078232; PubMed=2592374;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunodeficiency virus.";
Bur. J. Immunol. 22:2973-2981(1992)
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                                                                                                                                                                                                 PALMITOYLATION
                                                                                                                                                                                                                                   Nature
                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (3.9 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                           Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91061881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93049640; PubMed=1425921;
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                                                                                                                                                                                                                                                                                                                                                                                              "Crystal structure of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              K-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS)
FUNCTION: Accessory protein for MHC class-II antigen/
receptor interaction. May regulate T-cell activation.
SUBUNIT: Associates with p56-location.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: Contains 3 immunoglobulin-like C2-type dom
SIMILARITY: Contains 1 immunoglobulin-like V-type dom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       348:411-418(1990).
                                                                                                                                                                                                                                   387:527-530(1997).
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                                                                                                                                                                                                                                                                      segmental
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, Axel R
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CD4 molecules: diversity of
codeficiency virus/human
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between the Euro

European Bioinformatics Institute.

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WWW-"http://www.ncbi.nlm.nih

.gov/prow/cd/cd4.htm".

collaboration

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DATABASE: NAME=PROW; NOTE=CD guide CD4 entry,

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PDB; 1CDH; 30-APR-94.
PDB; 1CDI; 30-APR-94.
PDB; 1CDI; 31-APR-97.
PDB; 1CDJ; 01-APR-97.
PDB; 1WF0; 07-JUL-97.
PDB; 1WF0; 07-JUL-97.
PDB; 1WF0; 07-JUL-97.
PDB; 1WF0; 07-JUL-97.
PDB; 1GGN; 27-DEC-00.
PDB; 1GSN; 27-DEC-00.
PDB; 1GSN; 27-DEC-00.
PDB; 1GC1; 19-AUG-98.
PDB; 1GC1; 19-AUG-99.
PDB; 1GC1; 19-AUG-90.

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EMBL; W47924; AAB51309.1; -.
EMBL; W35160; AAA16069.1; -.
EMBL; M35160; AAA16069.1; -.
EMBL; M35160; AAA16069.1; -.
EMBL; M35160; AAA16069.1; -.
EMBL; BC025782; AAH25782.1; -
PIR; A90872; RWHUT4.
PDB; 1CDH; 30-APR-94.
PDB; 1CDL; 30-APR-97.
PDB; 1CDU; 01-APR-97.
PDB; 1MBR; 12-MAR-97.
PDB; 1WBR; 12-MAR-97.
PDB; 1G9M; 27-DEC-00.
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TRANSMEM
DOMAIN
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin domain; Transmembrane; Glycoprotein; T-cel
Immune response; Repeat; Signal; Lipoprotein; Palmitate;
Polymorphism.
25
SIGNAL
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458
T-CELL SURFACE GLYCOPROTEIN
CHAIN
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T-CELL SURFACE GLYCOPROTEIN
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T-CELL SURFACE GLYCOPROTEIN
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                                                                                                   IG-LIKE V-TYPE.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
N-LINKED (GLCNAC. . . . /FTId=CAR_000053.
N-LINKED (GLCNAC. . . . . /FTId=CAR_000054.
BY SIMILARITY.
S-palmitoyl cysteine.
S-palmitoyl cysteine.
R -> W (in OKT4-negative
                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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Matches 393
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                      01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
T.cell surface glycoprotein CD4 precursor (T-
                                                  Fomsgaard A., Hirsch V.M., Johnson P.R.;
"Cloning and sequences of primate CD4 molecules:
cellular receptor for simian immunodeficiency via
                                                                                                                                   "A CD4 domain important for outside the virus binding Cell 60:747-754(1990).
immunodeficiency virus.";
Eur. J. Immunol. 22:2973-2981(1992).
Eur. FUNCTION: Accessory protein for MHC class-II antigen/T-cell-
-!- FUNCTION: Accessory protein for MHC class-II activation.
                                                                                       MEDLINE=93049640;
                                                                                                  TISSUE=Blood
                                                                                                             SEQUENCE OF 26-424 FROM
                                                                                                                                                                       Camerini D., Seed
                                                                                                                                                                                MEDLINE=90182664;
                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                   NCBI_TaxID=9598;
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Pred. No. 1.4e
1; Mismatches
                                               immunodeficiency virus/human
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Catarrhini; Hominidae; Pan
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EMBL; X73323; CAA51749.1; -.
PIR; B32722; RWCZTA.
HSSP; P01730; 1WIQ.
G0; G0:0042101; C:T-cell recep G0; G0:0042101; C:T-cell recep G0; G0:0042505; F:MHC class II
G0; G0:0042505; P:immune respo G0; G0:0045086; P:positive reg G0; G0:0030217; P:T-cell diffe G0; G0:0005058; P:T-cell delec G0; G0:0015058; P:T-cell delec G0; G0:0015059; P:T-ansmembran G0; G0:0015059; P:T-ansme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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PRINTS; PR00692; CD4TCANTIGEN.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000973; CD4 TCAg.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR003596; Ig_v.
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GO:0042109; F:MC class II protein binding; ISS.
GO:0042209; F:MMC class II protein binding; ISS.
GO:0006955; P:immune response; ISS.
GO:0045086; P:positive regulation of interleukin-2 biosyn.
GO:0045081; P:T-cell differentiation; ISS.
GO:0045083; P:T-cell selection; ISS.
GO:0045084; P:transmembrane receptor protein tyrosine kin.
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SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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                                                                                                                     LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                      MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKS1QFHWKNSNQIK
                            TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                                                                                                                                                            ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                         MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQTK
                                                                                                                                                                                            ILGNOGSFLTKGPSKLNDRVDSRRSLWDQGNFTLIIKNLKIEDSDTYICEVGDQKEEVQL
Conservative
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98.2%;
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BY SIMILARITY.
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N-LINKED (GLCNAC...)
BY SIMILARITY.
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CS-palmitoyl cysteine (S-palmitoyl cysteine (S-palmitoyl Cysteine (S-palmitoyl Cysteine)
T-> N (IN REF. 2).
L-> S (IN REF. 2).
L-> N (IN REF. 2).
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CYTOPLASMIC (POTENTIAL).

IG-LIKE V-TYPE.

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.
                                                                                                                                                                                                                                                                                                                                                                                                                Score 2000; DB 1;
Pred. No. 4.7e-121;
1; Mismatches 6;
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CD4 MACFU

ID 4 MACFU

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R GO; GO:0015026; F:coreceptor activity; ISS.
R GO; GO:0015026; F:coreceptor activity; ISS.
R GO; GO:0042289; F:MHC class II protein binding; ISS.
R GO; GO:0042289; F:MHC class II protein binding; ISS.
R GO; GO:0045086; P:positive regulation of interleukin-2 binding; GO:0045017; P:T-cell differentiation; ISS.
R GO; GO:0030217; P:T-cell differentiation; ISS.
R GO; GO:0007169; P:T-cell delection; ISS.
R GO; GO:00045058; P:T-cell d
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P79184;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1-cell surface glycoprotein CD4 precursor (T-cell surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                       DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D63348; BAA09672.1; -. HSSP; P01730; 1WBR.
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-: FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation.

-: SUBUNIT: Associates with p56-lck (By similarity).

-: SUBCELLULAR LOCATION: Type I membrane protein.

-: SIMILARITY: Contains 1 immunoglobulin-like C2-type domains.
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Submitted (FEB-1997) to t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                 CHAIN
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Immunoglobulin domain;
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BY SIMILARITY.
T-CELL SURFACE GLYCOPROTEIN EXTRACELLULAR (POTENTIAL). POTENTIAL. CYTOPLASMIC (POTENTIAL).
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                                                                   MEDLINE=90182664; PubMed=2107024; Camerini D., Seed B.; "A CD4 domain important for HIV-mediated outside the virus binding site."; Cell 60:747-754(1990).
                                                                                                                                                                                            Macaca mulatta (Rhesus macaque)
Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Primates; C
Cercopithecinae; Macaca.
NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                  P16003; Q29617;
01-APR-1990 (Rel. 14, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
T-cell surface glycoprotein CD4 precursor (T-cell
SEQUENCE FROM N.A.
TISSUE=Thymocytes;
Hashimoto O., Tatsumi
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IG-LIKE C2-TYPE 1
IG-LIKE C2-TYPE 2
IG-LIKE C2-TYPE 3
N-LINKED (GLCNAC
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N-LINKED (GLCNAC
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Pred. No. 1.3e
18; Mismatches
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HSSP; P01730; IMBR.

GO; GO:0042101; C:T-cell receptor complex; ISS.
GO; GO:0015026; F:coreceptor activity; ISS.
GO; GO:0015026; F:coreceptor activity; ISS.
GO; GO:0042289; F:MHC class II protein binding; ISS.
GO; GO:0006955; P:immune response; ISS.
GO; GO:0045086; P:positive regulation of interleukin-2 bid GO; GO:0045018; P:T-cell differentiation; ISS.
GO; GO:0010217; P:T-cell differentiation; ISS.
GO; GO:0007169; P:T-cell selection; ISS.
GO; GO:0007169; P:T-cell selection; ISS.
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R GO; GO:0007169; P:T-cell selection; ISS.
R InterPro; IPR000973; CD4 TCAg.
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InterPro; IPR003596; Ig-V.
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Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig; 2.
PRINTS; PR00692; CD4TCANTIGEN
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin domain; Transm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M31134; AAA36838.1; -.
EMBL; D63347; BAA09671.1; -.
EMBL; X73326; CAA51752.1; -.
EMBL; AF057385; AAC25129.1;
EMBL; P01730; 1WBR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mol. Biol. Evol. 15:892-900(1998)
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                                                                                                                                                                                                                                                                                                                                                                                                         response;
         AAC25129.1; -.
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Repeat; Signal; Lipoprotein; Palmitate.
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CYTOPLASMIC (POTENTIAL).

IG-LIKE V-TYPE 1.

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IG-LIKE C2-TYPE 3.

IG-LIKED (GLCNAC. . .) (EN CLCNAC. . .) (EN C
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Best Local Similarity
Matches 357; Conserv
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NCBI_TaxID=9541;
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Tatsumi M., Yabe M.,
Submitted (FEB-1997)
                                                                                                                                                                                                                                                                                                               SEQUENCE
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15-JUL-1998 (Rel. 36, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
T-cell surface glycoprotein CD4 precursor (T-cell
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s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on ties by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial
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ata; Craniata; Vertebrata; Euteleostomi;
tes; Catarrhini; Cercopithecidae;
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Pred. No. 1.5e
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S -> P (IN REF. 2).
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GO; GO:0042102; F:coreceptor activity; ISS.
GO; GO:0042203; F:MCC class II protein binding; ISS.
GO; GO:0042203; F:MC class II protein binding; ISS.
GO; GO:0045086; P:positive regulation of interleukin-2 binding; GO:00030217; P:T-cell differentiation; ISS.
GO; GO:0030217; P:T-cell differentiation; ISS.
GO; GO:0045086; P:T-cell selection; ISS.
GO; GO:0045086; P:T-cell selection; ISS.
GO; GO:0045086; P:T-cell selection; ISS.
GO; GO:0007169; P:T-cell selection; ISS.
GO; GO:0007169; P:T-cell selection; ISS.
InterPro; IPR00073; CD4_TCA9.
InterPro; IPR000731; CJ4_TCA9.
InterPro; IPR000731; CJ4_TCA9.
InterPro; IPR000731; CJ4_TCA9.
InterPro; IPR000731; CJ4_TCA9.
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PRINTS; PR00692; CD4TCANILLUM.

SMART; SM00406; IGv; 1.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 1.

Immunoglobulin domain; Transmembrane; Glycoprotein;

Immunoglobulin domain; Transmembrane; Glycoprotein; Palmit

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HSSP; P01730; 1WBR.
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                              LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVEP
                                                                                                       LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
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  LNPEAGMWQCLLSDSGQVLLESNIKVVPTWPTPVQP
                                                                               LEAKTGKLHQEVNLVVMRATQFQENLTCEVWGPTSPKLTLSLKLENKGTTVSKQAKAVWV
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Pred. No. 2.3e-111;
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RESULT 6
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R EMBL; X73325; CAA51751.1; -.

R HSSC; P01730; 1WBR.

GO; GO:0042101; C:T-cell receptor complex; ISS.

GO; GO:0042101; C:T-cell receptor activity; ISS.

GO; GO:0015026; F:Correceptor activity; ISS.

GO; GO:0006955; P:MHC class II protein binding; ISS.

GO; GO:0006955; P:Immune regulation of interleukin-2 bio.

GO; GO:0045086; P:Positive regulation of interleukin-2 bio.

GO; GO:0030217; P:T-cell differentiation; ISS.

GO; GO:0007169; P:T-cell differentiation; ISS.

GO; GO:0007169; P:T-cell delection; ISS.

GO; GO:0007169; P:T-cell delection
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Q08340; P79196;
01-FEB-1995 (Rel. 31, Created)
15-JUL-1998 (Rel. 36, Last sex
10-OCT-2003 (Rel. 42, Last and
T-cell surface glycoprotein C)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -I- FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation.
-I- SUBUNIT: Associates with p56-lck (By similarity).
-I- SUBCELLULAR LOCATION: Type I membrane protein.
-I- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
-I- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. Hashimoto O., Tatsumi M.; Submitted (FEB-1997) to t
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Eur. J. Immunol. 22:2973-2981(1992)
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                                     LDAKTGKLHQEVNLVVMRATQFQENLTCEVWGPTSPKLTLSLKLENKGTTVSKQAKAVWV
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R EMBL; X73322; CAA51748.1; -.

R EMBL; AF001228; AAB60875.1; -.

R EMBL; AF001228; AAB60875.1; -.

R EMBL; AF001228; AAB60875.1; -.

R EMBL; AF07380; AAC25124.1; -.

R EMBL; AF07380; AAC25124.1; -.

R GO; GO:0042101; C:T-cell receptor complex; ISS.

R GO; GO:0042101; C:T-cell receptor in binding; ISS.

R GO; GO:0042289; F:MC class II protein binding; ISS.

R GO; GO:0042289; F:MC class II protein binding; ISS.

R GO; GO:0045086; P:Deositive regulation of interleukin-2 biosyn.

R GO; GO:0030217; P:T-cell differentiation; ISS.

R GO; GO:0030281; P:T-cell selection; ISS.

R GO; GO:0045088; P:T-cell selection; ISS.

R GO; GO:0045089; P:T-cell selection; ISS.

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EMBL; AF057380; AAC25124.1; -..
HSSP; P01730; IMIQ.
GO; GO:0042101; C:T-cell receptor
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TISSUE-Peripheral blood;

MEDLINE-98017879; PubMed-9379478;

MEDLINE-98017879; PubMed-9379478;

Fommsgaard A., Mueller-Trutwin M.C., Diop O., Ha

Corbet S., Barre-Sinoussi F., Allan J.S.;

"Relation between phylogeny of African green mo

their respective simian immunodeficiency virus
J. Med. Primatol. 26:120-128(1997).
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Mol. Biol. Evol. 15:892-900(1998).
-!- FUNCTION: ACCESSORY protein for MHC C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation. SUBUNIT: Associates with p56-lck (By similarity) SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: Contains 3 immunoglobulin-like C2-type domains. SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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Mammalia; Eutheria; I
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           immunodeficiency virus.";
Eur. J. Immunol. 22:2973-2981(1992)
-!- FUNCTION: Accessory
                                            Fomsgaard A., Hirsch V.M., Jo "Cloning and sequences of pricellular receptor for simian
                                                                               MEDLINE=93049640; PubMed=1425921;
                                                                                          TISSUE=Blood
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Obordata; Craniata; Vertebrata; Euteleostomi;
ia; Chordete; Catarrhini; Cercopithecidae;
Erythrocebus.

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    ycoprotein CD4 (T-cell surfa

                                            V.M., Johnson P.R.;
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R GO; GO:0042209; F:MCC class II protein binding; ISS.
R GO; GO:0042209; F:MFC class II protein binding; ISS.
R GO; GO:004508; P:Immune response; ISS.
R GO; GO:004508; P:positive regulation of interleukin-2 biosyn. . . .
R GO; GO:0030217; P:T-cell differentiation; ISS.
R GO; GO:0030217; P:T-cell selection; ISS.
R GO; GO:0007169; P:Transmembrane receptor protein tyrosine kin. . .
R GO; GO:007169; P:transmembrane receptor protein tyrosine kin. . .
R GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .
R GO; GO:007169; P:T-cell selection; ISS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIPID
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immune response; Repeat; Lipoprotein; Palmitate.
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SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: Contains 3 immunoglobulin-like C2-type domain
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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                                                                                      SSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSVKRVT
                QDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQKNLT
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S-palmitoyl cysteine (S-palmitoyl cysteine)
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GO; GO:0042289; F:MHC class II protein binding; ISS.
GO; GO:0042289; F:MHC class II protein binding; ISS.
GO; GO:0006955; P:immune response; ISS.
GO; GO:0003016; P:positive regulation of interleukin-2 biosyn. .
GO; GO:0030217; P:T-cell differentiation; ISS.
GO; GO:0030217; P:T-cell selection; ISS.
GO; GO:0045058; P:T-cell selection; ISS.
GO; GO:0007169; P:T-cell selection; ISS.
InterPro; IPR00731; CD4 TCAg.
InterPro; IPR003196; Ig_V.
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EMBL; X73327; CAA51753.1; -.
HSSP; P01730; 1WIQ.
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                                                                                                             PRINTS; PR00692; CD4
SMART; SM00406; IGV;
                                                                                                                                         Pfam; PF00047; ig;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; 
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; 
Cercopithecinae; Cercocebus.
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                                                        AMARI, WHATE, T. IG LIKE; 1.

ROSITE; PESSO835; IG LIKE; 1.

Immunoglobulin domain; Transmembrane;

Immune response; Repeat; Lipoprotein;
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3ur. J. Immunol. 22:2973-2981(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation. SUBUNIT: Associates with p56-lck (By similarity). SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: Contains 3 immunoglobulin-like C2-type domains. SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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                                                              Glycoprotein; T-cell; Palmitate.
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T-cell surface glycoprotein Cl
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Tatsumi M., Hashimoto O.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Accessory protein for MHC class-II antigen/T-cell
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae;
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IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
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Matches 30
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HSSP; P01730; IWBR.

GO; GO:0042101; C:T-cell receptor

GO; GO:0015026; F:Coreceptor activ

GO; GO:0015026; F:Coreceptor activ

GO; GO:0042289; F:MHC class II pro

GO; GO:0045086; P:Dostitive response;

GO; GO:0045086; P:T-cell different

GO; GO:0045086; P:T-cell different

GO; GO:0045058; P:T-cell selection

GO; GO:0041059; P:T-cell selection

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PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin domain; Transm
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  QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                                 TWKCTVFQHLELV-FEINIVVLAFQQASSTVYKKEGEQVEFSFPLAFAAETLTGSGELCW
                                                                              TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
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P:positive regulation of interleukin-2
P:T-cell differentiation; ISS.
P:T-cell selection; ISS.
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F:coreceptor activity; ISS.
F:MHC class II protein binding; ISS
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S-palmitoyl cysteine (By s:
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Pred. No. 3.2e-94; 
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P01857;
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21-JUL-1986 (Rel. 01, Last s
15-MAR-2004 (Rel. 43, Last a
19 gamma-1 chain C region.
                                                                                                                                                                                                            Ponsting1 H., Hilschmann N.;

"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. chymotryptic peptides of the H-chain, alignment of the tryp peptides and discussion of the complete structure.";

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                                     DISULFIDE BONDS.

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Intrachain disulfide bonds.";

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Edelman G.M.;
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MEDLINE-71064025; PubMed-5530842;
Rutishauser U., Cunningham B.A.,
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MEDLINE-82274238; PubMed=6287432;
 MEDLINE=77070267; PubMed=1002129,
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             SULFIDE BONDS
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Dreker L., Schwarz J., Reichel W., Hilschmann N.;
"Rule of antibody structure. The primary structure of a monoclonal
IgGl immunoglobulin (myeloma protein Nie), I: Purification and
characterization of the protein, the L- and H-chains, the
cyanogen bromide cleavage products, and the disulfide bridges.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
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Biochemistry 20:2361-2370(1981)
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G1M(1) markers, 239-D and 241-L. KOL and E
G1M(3) marker and the G1M (non-1) markers
MISCELLANDOUS: Nie also differs in the ami
35, 116, 198, 269 and 272.
MISCELLANDOUS: EV also differs in the amid
155, 166, 177, 195, 198, 269, and 272 and
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MISCELLANEOUS:
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MIM; 147100; -.
GO; GO:0005624; C:membrane fraction;
GO; GO:0003823; F:anntigen binding; Tr
GO; GO:0006955; P:lmmune response; Nr
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC. 3D-stricture.

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DISULFID PROSITE; Pfam; PF00047; ig; SMART; SM00407; IGc mmunoglobulin 1E4K; 1FCC; 1HZH; 1I7Z; 1D5B; 1D5I; 1D6V; 1DN2; SM00407; IGc1; 2. ; PS50835; IG_LIKE; 3. ; PS00290; IG_MHC; 2. lobulin domain; Immuno HGNC:5525; 15-JUL-92. 15-JUL-92. 12-NOV-97. 12-NOV-97. 09-PEB-00. 09-PEB-00. 04-OCT-00. 17-MAY-00. 17-MAY-01. 20-JUN-95. 20-JUN-95. 12-JUN-01. 16-MAY-01. 16-MAY-01. 16-MAY-01. 16-MAY-01. 16-MAY-01. 16-MAY-01. 16-MAY-01. 99 111 224 27 103 109 112 IGHG1. 98 110 223 330 83 103 109 112 Immunoglobulin fraction; INTERCHAIN INTERCHAIN INTERCHAIN CH1. HINGE CH2. CH3. NAS a region; Glycoprotein; HLIM) HLIM) HLIM) LIGHT HEAVY HEAVY CHAIN)

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                                                             SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
                                                                     SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
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                                                                                                                      VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK
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REMOVED POST: TRANSLATIONALLY.

K -> R (IN GIM(3) MARKER).

/FTId=VAR 003886.

D -> E (IN GIM(NON-1) MARKER).

/FTId=VAR 003887.

L -> M (IN GIM(NON-1) MARKER).

/FTId=VAR 003888.
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MIM; 147120; -.
GO; GO:0005624; C:membrane fraction
GO; GO:0003823; F:antigen binding;
GO; GO:0006955; P:immune response;
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_C1.

fraction;

EMBL;

; J00231; AAA52805.1; ; P01857; 1FC1. ;w; HGNC:5527; IGHG3. 147120; -.

.ch/announce/

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gene deletion model.";

Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).

-!- SUBUNIT: Dimer linked by 12 disulfide bonds; it interchain disulfide bond at position 7 in addit normally present in the hinge region.

-!- MISCELLANEOUS: The heavy chain disease protein WISCELLANEOUS: The sequence of residues 42-76 was a sequence of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986
21-JUL-1986
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1g gamma-3 cl
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MEDLINE-81021548; PubMed=6774747;

Frangione B., Rosenwasser E., Prelli
"Primary structure of human gamma 3 i
gamma 3 heavy-chain disease protein w
Biochemistry 19:4304-4308(1980).
This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alexander A., Steinmetz M., Barritault D., Franklin E.C., Hood L., Buxbaum J.N.; "Gamma Heavy chain disease in man: cDNA se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Michaelsen T.E., Frangione B., Franklin E.C.; Primary structure of the 'hinge' region of human IgG3. quadruplication of a 15-amino acid residue basic unit."; J. Biol. Chem. 252:883-889(1977).
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                               and all of the CHI region.

All of the CHI region, all miscritaneous: Disease protein ZUC lack most of the V region, all of the CHI region, and part of the hinge compared with normal the CHI region, and part of the hinge compared with normal gamma-3 heavy chains.

MISCELLANEOUS: Disease protein OMM may represent an allelic form or another gamma chain subclass.

MISCELLANEOUS: The hinge region in gamma-3 chains is about four times as long as in other gamma chains and contains three identical 15-residue segments preceded by a similar 17-residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ref 2.
MISCELLANBOUS: Disease protein
and all of the CH1 region.
nisease protein
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PROSITE; PS00290; IG_MHC; 1.

Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat;

Pyrrolidone carboxylic acid.
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                                                                                                     PMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPG
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Pred. No. 6.9e
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T -> A (IN OMM).
/FTId=VAR 003893.
S -> N (IN OMM).
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REMOVED POST-TRANSLATIONALLY
QV -> EB (IN ZHC)
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MISSING (IN ZUC).
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F -> Y (IN OMM).
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/FTId=VAR_003890.
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                                               PRT;
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Homo sapiens (Human)
Eukaryota; Metazoa; C
Mammalia; Eutheria; I
NCBI_TaxID=9606;
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SEQUENCE OF A
                                                                               Biochem.
                                                                                                                                                                                                                                      Stoppini M., Bellotti V., Negri A., "Characterization of the two unique immunoglobulins.";
                                                                                                                                                                                                                                                                                                                                                        REVISIONS TO 25; 59; 6
Hofmann T., Parr D.M.;
Submitted (MAR-1980) t
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=80114419; PubMed=118920; Hofmann T., Parr D.M.; "A note of the amino acid sequence immunoglobulins gamma chains."; Mol. Immunol. 16:923-925(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN MEDLLINE=80001357; PubMed=113060; Connell G.E., Parr D.M., Hofmann T; "The amino acid sequences of the three heavy domains of a human IgG2 myeloma protein."; Can. J. Biochem. 57:758-767(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL). MEDLINE=81007873; Pubmede-6774012; Wang A.-C., Tung E., Fudenberg H.H.; "The primary structure of a human IgG2 hea evolutionary, and functional implications. J. Immunol. 125:1048-1054(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Fetal liver;
MEDLINE=83001943; PubMed=6811139;
Takahashi N., Ueda S., Obata M., Nikaido
"Structure of human immunoglobulin gamma
evolution of a gene family.";
Cell 29:671-679(1982).
    MEDLINE=69064124; PubMe
Frangione B., Milstein
"Structural studies of
                                                                                                 MEDLINE=7203500; PubMed=4940472;
Milstein C., Frangione B.;
"Disulphide bridge of the heavy
Biochem. J. 121:217-225(1971).
                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-121 (DOT).
MEDLINE=95255298; PubMed=7737190;
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Hofmann T.
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"Comparison of the hinge-coding segments in human immunoglobulin gamma
heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
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"Linkage and sequence ho
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PubMed=5782707;
stein C., Pink J.R.L.
es of immunoglobulin
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GO; GO:0003833; F:antigen binding; TAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPRO07110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
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RESULT 14 CD4_RABIT

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HSSP; P01730; 1WBR.

GO; GO:0042101; C:T-cell receptor complex; ISS.
GO; GO:0015026; F:coreceptor activity; ISS.
GO; GO:0015026; F:coreceptor activity; ISS.
GO; GO:0042289; F:MHC class II protein binding; ISS.
GO; GO:0045085; P:jensitive regulation of interleukin-2 bid go; GO:0045086; P:positive regulation; ISS.
GO; GO:0030217; P:T-cell differentiation; ISS.
GO; GO:0030217; P:T-cell selection; ISS.
GO; GO:0045058; P:T-cell selection; ISS.
GO; GO:0045058; P:T-cell selection; ISS.
GO; GO:0007169; P:T-cell selection; ISS.
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor interaction. May regulate T-cell activation.
-!- SUBUNIT: Associates with p56-lck (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domains.
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01-NOV-1995 (Rel. 32, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
T-cell surface glycoprotein CD4 precursor (T-cell surface antigen
                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 2. TRINTS; PR00692; CD4TGEN SMART; SM00406; IGv; 1. PROSITE; PS50835; IG LIKE; 1. Immunoglobulin domain; Transmy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
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                                                                                                                       CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M92840; AAA31198.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hague B.F.,
Kindt T.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9986;
                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P46630;
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Proc. Natl. Acad. Sci. U.S.A. 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Accessory protein for MHC class-II receptor interaction
                                                                                                                                                                                                                                                                         response;
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                                           Sawasdikosol S.,
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                                                                                                                                                                                                                                                                       omain; Transmembrane; Glycoprotein; T-cell; Repeat; Signal; Lipoprotein; Palmitate.
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33.7%;
56.9%;
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IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
N-LINKED (GLCNAC...
                                          S-palmitoyl cysteine (By similarity)
S-palmitoyl cysteine (By similarity)
; B323311CBD40013D CRC64;
                                                                                         POTENTIAL.
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Score 1149; DB 1;
Pred. No. 1.7e-66;
                                                                                                                                                                                               POTENTIAL.
CYTOPLASMIC
                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL)
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              Length 459;
                                                                                                                       (POTENTIAL).
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1_HUMAN
GC4_HUMAN
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21-JUL-1986
21-JUL-1986
10-OCT-2003
                                                  This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                           MEDLINE=70207560; PubMed=4192699;
Pink J.R.L., Buttery S.H., de Vries G.M.,
"Human immunoglobulin subclasses. Partial
constant region of a gamma 4 chain.";
Biochem. J. 117:33-47(1970).
EMBL; K01316; AABS9394.1; ALT_INIT. PIR; A90933; G4HU. PDB; 1ADQ; 16-SEP-98.
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE=83157104; PubMed=6299662;

Ellison J.W., Buxbaum J.N., Hood L.E.;

Ellison d.W., Buxbaum J.N., Hood Inmunoglobulin

Nucleotide sequence of a human immunoglobulin

DNA 1:11-18(1981).
                                                                                                                                                                                                                                                                                                                                                       Eukaryota;
Mammalia; E
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-JUL-1986 (Rel. 01, Last sequence update)
-OCT-2003 (Rel. 42, Last annotation updat
gamma-4 chain C region.
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Primates;
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Best Local Sim
Matches 216;
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"Primary
Biochim.
[2]
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P33705;
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     SEQUENCE OF 13-463 FROM N.A.
STRAIN=Beagle; TISSUE=Thymus;
MEDLINE=93192324; PubMed=7916632;
MIDDE R.F., Conner G.E., Minz D.H., Alejandro R
"Primary structure of the canine CD4 antigen.";
Biochim. Biophys. Acta 1172:315-318(1993).
                                                                 Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                          01-FEB-1994 (Rel. 28, Last of 15-MAR-2004 (Rel. 43, Last of 15-cell surface glycoprotein
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SMART;
                                                            NCBI_TaxID=9615;
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DOMAIN
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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GO:0003823; F:antigen binding;
GO:0006955; P:immune response;
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PS50835; IG_LIKE; 3
PS00290; IG_MHC; 2.
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Matches 236
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EMBL; X68565; -
HSSP; P01730; 1
G0; G0:0015026;
G0; G0:0042289;
G0; G0:0042289;
G0; G0:0042289;
G0; G0:004289;
G0; G0:004289;
G0; G0:004289;
G0; G0:0045056;
G0; G0:0045056;
G0; G0:0045056;
G0; G0:0007169;
                                                                                              CARBOHYD
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SEQUENCE
                                                                                                                                   LIPID
LIPID
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                                                                                                                                                                                                                                                                                  TRANSMEM DOMAIN
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between
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tissue Antigens 43:184-188(1994).

-!- FUNCTION: Accessory protein for MHC class-II antige receptor interaction. May regulate T-cell activation. SUBUNIT: Associates with p56-1ck (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: Expressed in macrophages and a
                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0692; CD4TCF
SMART; SM00406; IGV; 1
                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000973; CD4 TCAg.
InterPro; IPR007110; Ig-Iv.e.
InterPro; IPR003596; Ig-v.e.
Pfam; PF00047; ig; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                       rкOSITE; PS50835; IG_LIKE; 1.
Immunoglobulin domain; Transm
                                                                                                                                                                                                                                                                                                                                              Immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO:0006955; P:immune response; ISS.
GO:0045086; P:positive regulation of interleukin-2 bic
GO:0030217; P:T-cell differentiation; ISS.
GO:0045058; P:T-cell selection; ISS.
GO:0007169; P:transmembrane receptor protein tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO:0042101; C:T-cell receptor complex; ISS.
GO:0015026; F:coreceptor activity; ISS.
GO:0042289; F:MHC class II protein binding; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Contains 3 immunoglobulin-like C2-type domain: SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lymphocytes.
                                                                                                                                                                                                                                                                                                                                              response; Repeat;
                                                           Similarity
 MNQEAAFRHLLLMLQLVMLPAVTPVREVVLGKAGDAVELPCQTSQKKNIHFNWRDSSMVQ
                 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                               AAB02295.1;
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                                                                                                                                                                                                                                                                                                                                                                                              CD4 TCANTIGEN
                                                                                                                      51639
                                                           33.4%;
57.6%;
                                                                                                                                                                                                                                                                                                                                           Transmembrane; Glycoprotein; T-cet; Signal; Lipoprotein; Palmitate.
                                                                                                ¥.
                                                63 ;
                                                                                             BY SIMILARITY.

BY SIMILARITY.

S-palmitcyl cysteine (B S-palmitcyl Cycteine (B N-LINKED (GLCNAC...)

N-LINKED (GLCNAC...)
                                             Score 1141; D
Pred. No. 5.6e
3; Mismatches
                                                                                                                                                                                                        IG-LIKE V-TYPE.
IG-LIKE C2-TYPE 1
IG-LIKE C2-TYPE 2
IG-LIKE C2-TYPE 2
IG-LIKE C2-TYPE 3
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                         EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S.P., Waldmann H.; encoding the canine
                                                                                                                                                                                                                                                                                                                      SURFACE GLYCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        There are no restrictions ong as its content is in
                                             DB 1;
.6e-66;
les 93;
                                                                                                                                                                                                                                                                                                          (POTENTIAL)
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                                                                    Length 463;
                                                                                                                                                                     (By similarity). (By similarity). .) (POTENTIAL).
                                               Indels
                                                                                                                     (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                         T-cell;
                                                                                                            (POTENTIAL)
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MBL outstation -
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SEQUENCE FROM N.A., AND PARLL....

MEDLINE=87175535; PubMed=3104900;
Clark S.J., Jefferies W.A., Barclay A.N., Ga "Peptide and nucleotide sequences of rat CD4"
Peyidence for derivation from a structure wit immunoglobulin-related domains.";
T immunoglobulin-related domains.";
Natl. Acad. Sci. U.S.A. 84:1649-1653(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD4 RAT
P05540;
01-NOV-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
T-cell surface glycoprotein CD4 precursor (T-cell 74/Leu-3) (W3/25 antigen).
                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                            Brady R.L., Dodson E.J., Dodson G.G., Lange G., Davis Williams A.F., Barclay A.N.; "Crystal Structure of domains 3 and 4 of rat CD4: rela NH2-terminal domains."; Science 260:979-983(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS)
MEDLINE=93262437; PubMed=8493535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat)
                                                                                                                                                                                FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction, May regulate T-cell activation.
SUBUNIT: Associates with p56-lck (By similarity).
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 1 immunoglobulin-like V-type domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVENLTAKWDSGSSGSSNIRLLQGQQLTLTLENPSGSSPSVQWKGPGNKSKHGGQNLSL
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Sciurognathi;
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CD4 (W3/25)
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EMBL; M15768;

A27449; 1CID; 1

A27449

AAA40901.1;

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GO; GO:0015026; F:coreceptor acceptor acceptor
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Best Local S
Matches 207
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G0; G0:0042101; C:T-cel
G0; G0:0015026; F:corec
G0; G0:0012289; F:MHC c
G0; G0:0042289; P:immur
G0; G0:0045086; P:Dosit
G0; G0:0030217; P:T-cel
G0; G0:0045058; P:T-cel
G0; G0:0045058; P:T-cel
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Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;
Immune response; Repeat; Signal; Lipoprotein; Palmitate; 3D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          response; Repeat;
                                                                                                                                                                Similarity
QLLVFGLTANSDTHLLQGQSLTLTLES-PPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQ
                                                     IKILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEV
                                           KTILGYKNKLLIKGSLELYSRFDSRKNAWERGSFPLIINKLRMEDSQTYVCELENKKEEV
                                                                                              MCRGFSFRHLLPLLLLQLSKLLVVTQGKTVVLGKEGGSAELPCESTSRRSASFAWKSSDQ
                                                                                                                      MNRGVPFRHL--LLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQ
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52.9%;
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IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.

N-LINKED (GLCNAC...)

N-LINKED (GLCNAC...)

N-LINKED (GLCNAC...)

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY

BY SIMILARITY

S-palmitoyl cysteine (
S-palmitoyl cysteine (
                                                                                                                                                Score 999; DB 1;
Pred. No. 6.9e-57;
1; Mismatches 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                       477BE157D30954C1 CRC64;
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CD4 MOUSE STANDARD; PRT; 457 AA.

P06332;
01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
T-cell surface glycoprotein CD4 precursor (T-cell surface
T4/Leu-3) (T-cell differentiation antigen L3T4).
                                                                                               Lu J., Gorz
Gibbs R.A.;
                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=98112780;
                                                                                                                                                                                                                                                                                                                                                                                                                           "L3T4 and the immunoglobulin gene between the immune system and the Immunol. Rev. 100:109-127(1987).
                                         "Comparative sequence analysis of a gene-rich cluster at human chromosome 12p13 and its syntenic region in mouse chromosome 6
                                                                                                                   Ansari-Lari M.A., Oel
Lu J., Gorrell J.H.,
                                                                                                                                                                                                                                   Proc.
                                                                                                                                                                                                                                                                                  "Structure of the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=88152875; PubMed=3326818; Parnes J.R., Hunkapiller T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Littman D.R., Gettner S.N.;
"Unusual intron in the immunoglobulin murine CD4 (L3T4) gene.";
Nature 325:453-455(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=87018845; PubMed=3094146;

Tourvieille B., Gorman S.D., Field E.H., Hunka

"Isolation and sequence of L3T4 complementary

in T cells and brain.";
                                                                                                                                                                                                                                                                                                                                MEDLINE=88041159; PubMed=2823269;
                                                                                                                                                                                                                                                                                                                                                             TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=87115821; PubMed=3027575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                              in brain."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLALEAKTGKLHQEVNLVVMRATQLQKN-LTCEVWGPTSPKLMLSLKLENKEAKVSKREK
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                                                                                                                                                                                                                                                                               Tourvieille B., the mouse gene
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                                                                                                           PubMed=9445485;
Oeltjen J.C., Schwartz
H., Chinault A.C., Belmo
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                                                                                                                     Belmont
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                                                                                                                J.W., M
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Miller W.,
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Schain M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Robastesin M.J., Uddin T.B., Toshiyuki S., Carrince P., H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Rodriguez A.C., Grimwood J., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schein J.E., Jones S.J.M., Marra M.A.;
Tenerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Thuman and mouse cDNA sequences S., Sanchez CDNA seq
                                                                  EMBL; M36850; AAA39401.1; -.
EMBL; M13816; AAA37767.1; -.
EMBL; M13816; AAA37767.1; -.
EMBL; M36851; AAA39402.1; -.
EMBL; M17080; AAA37403.1; -0.
EMBL; M17078; AAA37403.1; JOINED.
EMBL; M17079; AAA37403.1; JOINED.
EMBL; M17079; AAA37403.1; JOINED.
EMBL; M17079; AAA37403.1; JOINED.
EMBL; M17079; AAA37403.1; -.
EMBL; M17079; AAA37403.1; -.
EMBL; AC002397; AAC36010.1; -.
EMBL; BC039137; AAA439137.1; -.
EMBL; A02110; RWMST4.
HSSP; P01730; IWBR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-86233454; PubMed=3086886; Classon B.J., Tsagaratos J., McKenzie I.F.C., Walk Classon B.J., Tsagaratos J., McKenzie I.F.C., Walk Partial primary structure of the T4 antiques of massignment of intrachain disulfide bonds."; Proc. Natl. Acad. Sci. U.S.A. 83:4499-45031986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 27-43.
MEDLINE=86166694;
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STRAIN=C57BL/6J; TISSUE=Mammary gland;
MEDLINE=22388257; PubMed=12477932;
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GO:0042101; C:T-0
GO:0015026; F:CO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=P06332-2; Sequence=VSP_002489;
SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation. SUBUNIT: Associates with p56-lck (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=2; Synonyms=Brain-specific
IsoId=P06332-2; Sequence=VSP_(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Type ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way fied and this statement is not removed. Usage by and for commercial ties requires a license agreement (See http://www.isb-sib.ch/announce/end an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=P06332-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OF 27-43.
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I., TBagaratos J., Kirs
McKenzie I.F.C., Walk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23:129-132(1986).
C:T-cell receptor complex;
F:coreceptor activity; ISS
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Best Local
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InterPro; IPR003596; I
Pfam; PF00047; ig; 2.
PRINTS; PR00692; CD4TC
SMART; SM00406; IGv; I
PROSITE; PS50835; IG_I
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DISULFID
DISULFID
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TRANSMEM
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CARBOHYD
CARBOHYD
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DOMAIN
                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                         VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO:0042289;
GO:0006955;
GO:0045086;
GO:0030217;
GO:0045058;
GO:0007169;
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356
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                                                                                                                                                             117
                                                                                                                                                                              61
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                                                                                                                                                                                                                 _
                                                                                                                                                                                                                                                            Similarity
KVVQVVAPETGLWQCLLSEGDKVKMDSRIQVL
               KPVWVLNPEAGMWQCLLSDSGQVLLESNIKVL
                                            NLTLALEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKRE
                                                                               GELWWQAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSG
                                                                                                                  LQDSGTWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGS
                                                                                                                                          EVELWVFKVTFSPGTSLLQGQSLTLTLDSNSKVSNPLTECKHKKGKVVSGSKVLSMSNLR
                                                                                                                                                    EVQLLVFGLTANSDTHLLQGQSLTLTLES-PPGSSPSVQCRSPRGKNIQGGKTLSVSQLE
                                                                                                                                                                              KILGOHGKGVLIRGGSPSOF-DRFDSKKGAWEKGSFPLIINKLKMEDSOTYICELENRKE
                                                                                                                                                                                              KILGNOG-SFLTKG--PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKE
                                                                                                                                                                                                                 MCRAISLRRLLLLLLQLSQLLAVTQGKTLVLGKEGESAELPCESSQKKITVFTWKESDQR
                                                                                                                                                                                                                                   MNRGVPFRH-LLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQI
                                                                      GELMWKAEKDSFFQPWISFSIKNKEVSVQKSTKDLKLQLKETLPLTLKIPQVSLQFAGSG
                                                                                                      VQDSDFWNCTVTLDQKKNWFGMTLSVLGFQSTAITAYKSEGESAEFSFPLNFAEE--NGW
                                                                                                                                                                                                                                                                                       457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aplicing
                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                         $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F:MHC class II protein binding;
P:Immune response; ISS.
P:Dositive regulation of interle
p:T-cell differentiation; ISS.
P:T-cell selection; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P:transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CD4TCANTIGEN
                                  KGTLHQEVNLVVMKVAQLNNTLTCEVMG
                                                                                                                                                                                                                                                                                                         29.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane; Glycoprotein; T-cell; t; Signal; Lipoprotein; Palmitate;
                                                                                                                                                                                                                                                                                      ₩.,
                                                                                                                                                                                                                                                     62;
                                                                                                                                                                                                                                                                                     S-palmitoyl cysteine
S-palmitoyl cysteine
S-palmitoyl cysteine
Missing (in isoform 2)
/FTId=VSP 002489.
W; 1B1DA7527CB00F33 CRO
                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
CYTOPLASMIC (POTI
IG-LIKE V-TYPE.
IG-LIKE C2-TYPE
IG-LIKE C2-TYPE
IG-LIKE C2-TYPE
                                                                                                                                                                                                                                                                                                                                                            N-LINKED
N-LINKED
                                                                                                                                                                                                                                                           Score 993;
Pred. No. 1
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                                  PTSPKMRLTLKQENQEARVSEEQ
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RESULT 19 GC3M_MOUSE

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23-OCT-1986
01-AUG-1991
15-JUL-1999
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01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
15-JUL-1999 chain C region, membrane-bound f
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Ver
                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR007110; Ig-11ke. InterPro; IPR003597; Ig_G1. InterPro; IPR00306; Ig_MHC. Pfam; PF00047; Ig; 3. SMART; SM00407; IGG1; 2.
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EMBL; V01526; CAA24767.1; ALT_SEQ.
PIR; A02156; G3MSM.
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Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine IgG3 constant region gene.
                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 328-398 FROM N.A. MEDLINE-84041483; PubMed-6314258;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The structure of the mouse immunoglobulin in gamma 3 membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Komaromy M., Clayton L., Rogers
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                                                                                                                                                                                                                                                                                                                  mmunoglobulin domain; Immunoglobulin C region; Glycoprotein;
              481
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VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN
                                                                                                        SNIKVLPTWSTPVEPKSCDKTH---
                                               LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
                                                                                 SSLVTVPSSTWPSQTVICNVAHPASKTELIKRIEPRIPKPSTPPGSSCPPGNILGGPSVF
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E -> G (IN REF. 2).
E -> F (IN REF. 2).
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Pred. No. 1.2e-53;
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HINGE.
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                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                 "Gene segments encoding transmembrane immunoglobulin gamma chains."; Cell 26:19-27(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T. Takahashi N., Mano Y.; Takahashi N., Mano Y.; "Cloning and complete nucleotide sequence of mouse gamma 1 chain gene."; Cell 18:559-568(1979).
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01-AUG-1991 (Rel. 19, Last
10-OCT-2003 (Rel. 42, Last
Ig gamma-1 chain C region,
                                                                                                                                                                                                                                                                           Yamawaki Kataoka Y., Nakai S., Miyata T., Honjo T "Nucleotide sequences of gene segments encoding m immunoglobulin gamma chains.",
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
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Eisenberg D., Wall R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., "mRNA for surface immunoglobulin gamma chains encodes conserved transmembrane sequence and a 28-residue into
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                   Name=Membrane-bound
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                                                                                                                                                                        Note=May be the major isoform;
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19, Last sequence update)
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42, membrane-bound f
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EMBL; V00793; CAA24172.1; -. EMBL; V00793; CAA24173.1; -. EMBL; V00793; CAA24174.1; -.

entities requires a license agreement (Some send an email to license@isb-sib.ch).

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PDB; 1AE6; 18-MAR-98.

PDB; 1CT; 12-JAN-00.

PDB; 1F11; 06-FEB-01.

PDB; 1F58; 29-DEC-99.

PDB; 1KCR; 11-MAY-02.

PDB; 1KCR; 11-MAY-02.

PDB; 25CB; 09-JUL-99.

MGD; MGI:96446; Igh-4.

InterPro; IPR0077110; Ig-1ike.

InterPro; IPR003597; Ig_C1.

InterPro; IPR003006; Ig_MHC.

Pfam; PF000477; IGC1; 2.

SMART; SM004407; IGC1; 2.
  GC RABIT STANDARD; PRT; 323 AA.

PDIB70;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
11 gamma chain C region.
12 gamma chain C region.
Oryctolagus cuniculus (Rabbit).
Cukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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// MART; bmuvuv; AVC;
// ROSITE; PS50835; IG_LIKE; 3.
// PROSITE; PS00290; IG_MHC; 1.
// Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
// Immunoglobulin domain; Transmembrane; 3D-structure.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 3.
SMART; SM00407; IGcl; 2.
PROSITE; PS0035; IG_MHC; 1.
PROSITE; PS00290; IG_MHC; 1.
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Hill R.L., Lebovitz H.E., Fellows R.E. Jr.,
(In) Killander J. (eds.);
Gamma globulins, Nobel symp. 3, pp.109-127,
Stockholm (1967).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE=83299917; PubMed=6193512;
Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
"Heavy chain genes of rabbit IgG: isolation of a cDNA encoding
heavy chain and identification of two genomic C gamma genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
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SEQUENCE FROM N.A.
MEDLINE=84030930; PubMed=6313520;
Bernstein K.E., Alexander C.B., M
                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A91749; GHRB.
HSSP; P01857; 1FC1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-128.
MEDLINE=76135469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M16426; AAA31289.1; -.
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                                                                                                                                                                                                                                                                                     [mmunoqlobulin
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Biochem. J. 116:249-259(1970).
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       88-266 FROM N
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                                                                                                                                                                                                                                                                                     domain;
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         Ig-like.
Ig_cl.
Ig_MHC.
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IG-LIK
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(IN E15 MARKER).
(IN REF. 2).
V (IN REF. 2).
(IN REF. 3 AND 4).
(IN REF. 5).
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5 (IN REF. 5).
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Best Local S
Matches 169
EMBL; J00471; AAB59661.1; A
PIR; A02154; G2MSAM.
PDB; 1KB5; 08-APR-98.
PDB; 1YEB; 15-OCT-97.
MGD; MGI:96443; Igh-1.
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                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collabbetween the Swiss Institute of Bioinformatics and the EMBL outst. the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL 1986 (Rel. 01, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig gamma-2A chain C region, membrane-bound fo
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                              IsoId=P01864-1; Sequence=External;
Note=Probably the major isoform;
SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                   ALTERNATIVE PRODUCTS
                                                                                                                                                                                                                                                                                                                            Name=Secreted;
                                                                                                                                                                                                                                                                                                                                        Name=Membrane-bound;
IsoId=P01865-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=2;
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Pred. No. 3.8e
30; Mismatches
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1. 79:2623-2627(1982).
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RESULT 23
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Best Local Similarity
Matches 183; Conserv
                                 GC2 CAVPO STANDARD; PRT; 329 AA. P01862;
P01862;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 04, Last sequence update)
11-JUL-1999 (Rel. 38, Last annotation update)
115-JUL-1999 (Rel. 38, Cast annotation update)
12 gamma-2 chain C region.
Cavia porcellus (Guinea pig).
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; [Mammalia; Eutheria; Rodentia; Hystricognathi; Caviid
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                    NCBI_TaxID=10141;
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SMART; SM00407; IGcl; 2.

PROSITE; PS50835; IG_LIKE; 3.

PROSITE; PS00290; IG_MHC; 1.

Immunoglobulin domain; Immunoglobulin

Transmembrane; Alternative splicing; 3
SEQUENCE OF 1-3. Trischmann T.M.;
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                                                                                                                                                                             GELDGLWTT
                                                                                                                                                                                                                                                                       AKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVL
                                                                                                                                                                                                                                                                                                                                                                                                                                              PQALPQYAGSGNLTLALEAKTGKLHQEV-----NLVVMRATQLQKNLTCEVWGPTSPKLM
                                                                                                                                                                                                GELDGLWTT
                                                                                                                                                                                                                                DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQD
                                                                                                                                                                                                                                                                                                                  DKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
                                                                                                                                                                                                                                                                                                                                                                                                            LSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVEPKSC
                                                                                                                                                                                                                     DSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGLDLDDVCAEAQD
                                                                                                                                                                                                                                                              PKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVL
                                                                                                                                                                                                                                                                                                                                                                                          PEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPAS----
                                                                                                                                                                                                                                                                                                      VNNVEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR007110;
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Ig_cl.
Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERCHAIN
INTERCHAIN
INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IG-LIKE
IG-LIKE
IG-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 915.5; DB 1
Pred. No. 1.3e-51;
9; Mismatches 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERCHAIN
                                       Hystricognathi; Caviidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   921
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3D-structure;
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HEAVY
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CHAIN)
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                                                                                                                                  Query Match
Best Local :
                                                                                              Matches
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"Structure of heavy chain from strain 13 guinea immunoglobulin-G(2). II. Amino acid sequence of and hinge region cyanogen bromide fragments."; Biochemistry 10:9-17(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structure of heavy chain from strain 13 guinea immunoglobulin-G(2). 3. Amino acid sequence of the half-cystine joining heavy and light chains."; Biochemistry 10:18-25(1971).
                                                                                                                                           DISULFID
CARBOHYD
DISULFID
                                                                                                                                   SEQUENCE
                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                          Pfam; PF00047; ig; 2.
SMART; SM00407; IGc1; 2.
                                                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                        PIR; A94553; GZGP.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                    Biochemistry 10:26-31(1971).
-!- MISCELLANEOUS: This chain was
                                                                                                                                                                                                                                                                                                                                                                                                       Biochemistry 13:4804-4811(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochemistry 13:4796-4803(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=75036072; PubMed=4429665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 4-68. MEDLINE=71058471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (APR-1975)
[2]
                                                                                                                                                                        DISULFID
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                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                       Immunoglobulin
NON_TER
                                                                                                                                                                                                                                        PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 227-311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tracey D.E., Cebra J.J.;
"Primary structure of the CH2 homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 134-226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=71058486; PubMed=5538616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 69-133 AND
                                                                                                                                                                                                                                                                                                                                                      Dliveira B., Lamm M.E.;
"Interchain disulfide bridges of guinea
                                                                                                                                                                                                                                                                                                                                                                                                                          "Primary structure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                    Trischmann T.M., Cebra
                                                                                                                                                                                                                                                                                                                                                                                     SULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                           13 inbred guinea pigs.
                                     385
445
                  98
                                                        64
                                                                                                      Similarity
                                                                         NLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNI 384
                 PS50835; IG_LIKE; 3. PS00290; IG_MHC; 1.
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VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN 504
                                                       SLTSMVTVPSSQKATCNVAHPASSTKVDKTVEPI----
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28
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107
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142
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248
                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=4609467;
Cebra J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=5538606;
                                                                                                                                                                                                                                                                                                                                                                           PubMed=4922544;
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58.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                         CH3 homology
                                                                                           ; Score 906.5; ; Pred. No. 3.8e 31; Mismatches
                                                                                              31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR data bank.
                                                                                                                                                     N-LINKED
                                                                                                                                                                                  INTERCHAIN
                                                                                                                                                                                                             INTERCHAIN (WITH A LIGHT CHAIN)
                                                                                                                                                                        INTERCHAIN
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                                                                                                                                                                                                                                                                                                                                     isolated
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                                                                                                                                                     (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                         region from guinea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         region from guinea pig
                                                                                                                                                                                                                               region;
                                                                                                                                                                                                                                                                                                                                                        pig gamma-2-immunoglobulin.";
                                                                                                                                                                       HLIM)
HLIM)
HLIM)
                                                                                                      .8e-51;
                                                                                                               DB 1;
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                                                                                                                                                                       CHAIN)
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                                                                                                                                                                                                                                                                                                                                                                                                                         pig
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                                                                                            39;
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                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 335-405 FROM N.A. MEDLINE=82222190; PubMed=6283537; Yamawaki Kataoka Y., Nakai S., Mi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation updat
Ig gamma-2B chain C region, membrane-bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                   EMBL; J00462; AAB59659.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=82115295; PubMed=6799207;
Rogers J., Choi E., Souza L., Carter C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P01867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCBM MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell 26:19-27(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eisenberg D., Wall R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 335-378 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Nucleotide sequences of gene segments immunoglobulin gamma chains."; Proc. Natl. Acad. Sci. U.S.A. 79:2623-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           mmunoglobulin gamma chains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Gene segments encoding transmembrane carboxyl termini
                                                                                                                                                                                                                                                               Isoid=P01866-1; Sequence=External;
Note=May be the major isoform;
Note=May be the major isoform;
PTM: DISULFIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA CHAINS
MISCELLANEOUS: The sequence of residues 1-335 is assumed to
identical with the corresponding region of the secreted for
MISCELLANEOUS: The a allel sequence is shown.
SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                                                                                                                                                                                                                                                                                     Name=Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                              ALTERNATIVE PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                                  Name=Membrane-bound
                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2;
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                                                                                                    C02154;
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                                                                                                                                                                                                                                                                                                                                                                                   IsoId=P01867-1;
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                                                                                                    G2MSBM
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                                                                                                                  ALT_INIT
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A. 79:2623-2627(1982)
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MGD; MGI:96445; Igh-3. InterPro; IPR007110; Ig InterPro; IPR003597; Ig InterPro; IPR003006; Ig Pfam; PF00047; ig; 3.

Ig-like. Ig_c1. Ig_MHC.

1CIC; 11-MAR-03

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GCS MOULT GCS MOULT ID GCS MOULT GCS
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                                                                                                                                                                         GC3 MOUSE STANDARD; PRT; 329 AA.

ID GC3 MOUSE STANDARD; PRT; 329 AA.

C P2436;

T 01-AUG-1991 (Rel. 19, Last sequence update)

T 16-CCT-2001 (Rel. 40, Last annotation update)

E 19 gamma-3 chain C region, secreted form.

S Mus musculus (Mouse).

Elkaryota; Metazoa; Chordata; Craniata; Verteb.

Mammalia; Eutheria; Rodentia; Sciurognathi; Mull TaxID=10090;

[1]
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Best Local S
Matches 174
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Alternative spil
NON TER 1
DOMAIN 127
DOMAIN 235
DISULFID 15
DISULFID 109
DISULFID 119
DISULFID 115
DISULFID 116
DISULFID 117
DISULFID 118
DISULFID 118
DISULFID 118
DISULFID 150
DISULFI
                     SEQUENCE FROM N.A.
MEDIJIRE=85027161; PubMed=6092053;
Wels J.A., Word C.J., Rimm D., Der-
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine
EMBO J. 3:2041-2046(1984).
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PS00290; IG_MHC; 1.
bulin domain; Immunoglobulin
ive splicing; 3D-structure; Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
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Pred. No. 1.3e-49;
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CYTOPLASMIC (POTENTIAL).
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IG-LIKE 2.
IG-LIKE 3.
INTERCHAIN
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                                                                                                    Der-Balan
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                                                                                                 G.P.,
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                                                                                                    Martinez
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RESULT 2
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Best Local S
Matches 154
                                                                                       Ig gamma-2B chain C region.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Rodentia; S,
NCBI_TaxID=10116;
[1]
                                                                                                                                                    GCB RAT STAN
P20761;
01-FEB-1991 (Rel. 1
01-FEB-1991 (Rel. 1
10-OCT-2003 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane;
NON_TER 1
DOMAIN 1
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DOMAIN
DOMAIN
SEQUENCE
Gene 74:473-482(1988).

-- SIMILARITY: Contains 3 immunoglobulin-like

PIR; PS0018, PS0018.

HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                          MEDLINE=89232738; Publ
Brueggemann M.;
"Evolution of the rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig; 3.
SMART; SM00407; IGc1; 2
                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin
Transmembrane; Alternative splicing.
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PIR; B02156; G3MSC.
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Pro; IPR007110; Ig-like.
Pro; IPR003597; Ig_c1.
Pro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                        124
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114
224
329
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                                                                                                                                                                                                 STANDARD;
                                                                 PubMed=3149946;
                                                                                                                                                     17, Created)
17, Last sequence up
42, Last annotation
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113 H:
223 CI
327 CI
; 36228 MW;
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                                           immunoglobulin
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HINGE.
CH2.
CH3.
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2; Mismatches
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Pred. No. 1.
                                                                                                           Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                 PRT;
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on update)
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                                            heavy-chain
                       domains
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                                                                                                            Murinae;
                                            gene
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tions on its
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Best Local Similarity
Matches 153; Conserv
                                                                                                                                                                                                                    RAT 27
                                                                                                                                     01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence upd.
15-JUL-1999 (Rel. 38, Last annotation up.
15 gamma-1 chain C region.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata;
Manmalia; Eutheria; Rodentia; Sciurognat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig cl.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 3.
SMART; SM00407; IGcl; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG MIC; 1.
Immunoglobulin domain; Immunog
       PIR; PS0017; PS0017.
HSSP; P01847; 7FAB.
InterPro; IPR007710; Ig-like.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 3.
SMART; SM00407; IGC1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunoglobulin on NON TER 1
DOMAIN 124
DOMAIN 232
DISULFID 156
DISULFID 106
DISULFID 109
DISULFID 119
DISULFID 117
DISULFID 117
DISULFID 117
DISULFID 133
SEQUENCE 333
                                                                                                                                                                                                       GC1_RAT
P20759;
                                                                                Brueggemann M.;
"Evolution of the rat immunoglobulin
                                                                                                   SEQUENCE FROM N.A. MEDLINE=89232738;
                                                                                                                             NCBI_TaxID=10116;
                                                                       74:473-482 (1988) .
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PS50835;
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Best Local
Matches 19
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MEDLINE=80045036; PubMed=115593;
HONJO T., Obata M., Yamawaki-Kataoka Y
Takahashi N., Mano Y.;
"Cloning and complete nucleotide sequer
gamma 1 chain gene.";
Cell 18:559-568(1979).
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1_MOUSE
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                                                         MEDLINE=80202559; PubMed=6769752;
Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T
Obata M., Yeidman J.G., Peterlin B.M., Leder P., Honjo
Mano Y., Seidman J., Peterlin B.M., Leder P., Honjo
"Immunoglobulin gamma I heavy chain gene: structural g
cloned in a bacterial plasmid.";
Gene 9:87-97(1980).
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalla; Eutheria; Rodentia; NCBI_TaxID=10090; [1]
  SEQUENCE OF 70-322 FROM N.A. (MYELOMA MEDLINE=80012837; PubMed=113776;
                                                                                                                                                                                     SEQUENCE OF 76-324 FROM N.A. (MYELOMA
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No. 4.1e-46;
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Query Match
Best Local Similarity
Matches 144; Conser
                                                                                                                                                                                                                                                                                                                                                       EMBL; V00793; CAA24172.1; -.
EMBL; V00793; CAA24174.1; -.
EMBL; V00793; CAA24174.1; -.
EMBL; V00793; CAA24175.1; -.
EMBL; V00795; CAA24176.1; -.
PIR; A02159; GIMS.
                                          DISULFID
MOD_RES
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Svasti J., Milstein C.;
"The disulphide bridges of a mouse immunoglobulin Biochem. J. 126:837-850(1972).
-I- SUBCELIULAR LOCATION: Secreted.
-I- ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                                                              InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig c1.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 2.
SMART; SM00407; IGc1; 2.
                                                                                                                                                                                                                                                          SMART; SM00407; IGC1; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rogers J., Clarke P., Salser W.; "Sequence analysis of cloned cDNA encoding part of an
                                                                                                          CARBOHYD
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                                                                                                                                                                                                                                                                                                                                             GlycoSuiteDB; P01868; -.
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N -> D (IN REF. 3).
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Score 826.5; DB
Pred. No. 5e-46;
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma-2C chain C region.
Rattus norvegicus (Rat)
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                                                                                                                                        DOMAIN
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SMART; SM00407; IGc1; 2.
SMOSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                           EMBL; X07189; CAA3010
PIR; S00847; S00847.
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                                                                                                                                                                                                                                                                                                                                                                                                                        region cDNA: extensive homology to mouse gamma Eur. J. Immunol. 18:317-319(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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Score 817.5; DB 1
Pred. No. 1.9e-45;
6; Mismatches 51
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ramma 3.";
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21-JUL-1986
15-MAR-2004
                                                                                                            between
the Euro
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EMBL; J00479; -; NOT_ANNOTATED_
PIR; A02153; G2MGAB.
PDB; 1BOG; 23-MAR-99.
PDB; 1HH6; 26-JAN-01.
                                                                       use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
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9
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MEDLINE=82037777; PubMed=6794027;
                                                                                                                                                                                                                                                                                                                                                                                    Schreier P.H., Bothwell A.L.M., Mueller-Hill B., "Multiple differences between the nucleic acid sor IgGzaa and IgGzab alleles of the mouse."; Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499 (1981).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P01864;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=82037861; PubMed=6170065;
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s musculus (Mouse)
                                                            send an email to license@isb-sib.ch).
                                                                                                                                                      Name=Membrane-bound;
IsoId=P01865-1; Sequence=External;
ISOId=P01865-1; Sequence differs from that of the MISCELLANEOUS: The sequence differs from that of the from BALB/c mice, at 15% of the positions.
SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                            European Bioinformatics Institute.
                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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21-JUL-1986
21-JUL-1986
10-OCT-2003
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PDB; 1H16; 08-FEB-01.
InterPro; IPR007110;
InterPro; IPR003597;
InterPro; IPR003006;
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SEQUENCE
          MEDLINE=81198976; PubMed=6262729;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;
"The complete nucleotide sequence of mouse i
and evolution of heavy chain genes: further
sequence mediated domain transfer.";
                                                                                                                                                                                                      Sikorav J.-L., Auffray C., Rougeon F.; "Structure of the constant and 3' untranslated
                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=81076554; PubMed=6777755;
                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa;
Mammalia; Eutheria;
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation updat
Ig gamma-2A chain C region, A allele.
Ig samma-2N (Mouse).
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SMART; SM00407; IGC1; 2.
PROSITE; PS50835; IG LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin
                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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Nucleic Acids Res. 8:3143-3155(1980).
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08-FEB-01.
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Rodentia;
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; Ig_cl.
; Ig_MHC.
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IG-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 816;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                      mouse immunoglobin further evidence for
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les 86;
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SMART; SM00407; 1Gc1; 2. .
PROSITE; PS50835; IG LIKE; 3. PROSITE; PS00290; IG_MHC; 1.
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PIR; A02152; G2MSA.
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PDB; 1E4X; 12-JUL-01.
PDB; 1MNU; 06-MAY-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          de Preval C., Fougereau M.;
"Determination of the primary structure of a mouse gamma Gimmunoglobulin. Identification of the disulfide bridges.";
Eur. J. Blochem. 30:452-462(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bourgois A., Fougereau M., Rocca-Serra J.;
"Determination of the primary structure of a mouse IgG2a immunoglobulin:amino-acid sequence of the Fc fragment. Implication the evolution of immunoglobulin structure and function.";
Eur. J. Biochem. 43:423-435(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain suggests that exons can be exchanged between genes in a multiger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=81223894; PubMed=6787604; Ollo R., Auffray C., Morchamps C., Formarison of mouse immunoglobulin
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
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                                                                                                                                                                                                           Local
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SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                          340
 400
                                       90
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DKTHTCPP---CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY 457
                                                                      LSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVEPKSC
                                                                                                                                          PQALPQYAGSGNLTLALEAKTGKLHQEV-----NLVVMRATQLQKNLTCEVWGPTSPKLM
                                   PEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPAS----
                                                                                                                                                                                                                                                              250
330
330 AA;
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112
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220
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1112
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308
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                                                                                                                                                                                   47;
                                                                                                                                                                                                     Score 814.5;
Pred. No. 3e-
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INTERCHAIN
INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                                                                            IG-LIKE 1.
IG-LIKE 2.
IG-LIKE 3.
INTERCHAIN
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B84361C5445A6864 CRC64;
                                                                                                                                                                                       Mismatches
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375 SGQVLLESNIKV-LPTWST---

-PVEPKSCDK---THTCPP--CPAPELLGGPSV 419

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P20760;
01-FEB-1991 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation updat
Ig gamma-2A chain C region.
Rattus norvegicus (Rat)
                                               SEQUENCE
                                                                                                                                                                  NON TER
                                                                                                                                                                                                           Pfam; PF00047; ig; 2.
SMART; SM00407; IGc1; 2.
                                                                                                                                                                                                                                                                PIR; PS0019; PS0019.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                   EMBL; M13804; AAA41376.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                            Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                              DOMAIN
                                                                                                                                                        DOMĀIN
                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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                                                                                                                                                                             [mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                             Evolution of the rat immunoglobulin gamma heavy-chain sene 74:473-482(1988).
-!- SIMILARITY: Contains 3 immunoglobulin-like domains.
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              Similarity
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PS00290; IG_MHC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL
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221
27
102
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136
    Conservative
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212
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                                              35186 MW;
             23.3%;
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Score 795; DB 1; Lei
; Pred. No. 5.2e-44;
   39;
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Eukaryota; Metazoa; Chordata; C. Mammalia; Eutheria; Rodentia; S.
                                                                    Irimura T., Takahashi N., Matsunaga C., Yamamoto K., Irimura T., Takahashi N., Kato K., Arata Y.; "O-glycosylation in hinge region of mouse immunoglobulin G2b."; J. Biol. Chem. 269:12345-12350(1994). "I- SUBCELLULAR LOCATION: Secreted (Potential)."
-I- SUBCELLULAR LOCATION: Secreted (Potential).
-I- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=BUUDLOC,
Tucker P.W., Marcu K.B., Newell N., "
"Sequence of the cloned gene for the
"Sequence of the cloned years.";
                                                                                                                                                                                                                                                      CARBOHYDRATE-LINKAGE SITE THR-105.
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=82173203;
Ollo R., Rougeon |
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tucker P.W., Marcu K.B., Slightom J.L., "Structure of the constant and 3' untra gamma 2b heavy chain messenger RNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cloned from newborn nous
Nature 283:786-789(1980)
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"Complete nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tucker P.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=80081501; PubMed=117548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunoglobulin heavy chai
lence 206:1303-1306(1979).
                                                                  Event=Alternative
                                               Name=Secreted
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                                                                                                                                                                                                                                                                                              immunoglobulin allotypes: gamma 2b chain genes."; 296:761-763(1982).
                          :soId=P01866-1;
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206:1299-1303(1979).
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PubMed=6766534;
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  Sequence=Displayed;
major isoform;
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Sciurognathi; Muridae;
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IsoId=P01867-1; Sequence=External;

IsoId=P01867-1; Sequence=External;

IsoId=P01867-1; Sequence=External;

IsoId=P01867-1; Sequence=External;

IsoId=P01867-1; Sequence is shown.

IsoId=LANEDUS: The a allele sequence is shown.

IsoId=RITY: Contains 3 immunoglobulin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00407; IGC1; 2.
PROSITE; PS50835; IG_LIKE;
PROSITE; PS00290; IG_MHC; 1
Immunoglobulin domain; Immu
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HSSP; P01842; 7FAB.
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SMART; SM00407; IGc1
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InterPro; IPR003597;
InterPro; IPR003006;
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                                                                                                                                                                                                            NVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIK
                                                                                                                                                                                                                                                                           LSLXLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVEPKSC 399
                                                                                                               DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                   DGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPG
                                                                                                                                                 GLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDS
                                                                                                                                                                               GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
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l; Mismatches
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STANDARD;

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P01873;
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01-NOV-1991 (Rel. 20, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation updat
Ig mu chain C region membrane-bound form.
Mus musculus (Mouse).
                                                                                                                                                                                              PROSITE; PS50835; IG_LIKE; 4. PROSITE; PS00290; IG_MHC; 3. Immunoglobulin domain; Immuno
                                                                                                                                                                                                                            InterPro; IPR007110; Ig-1ike.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR00306; Ig_MHC.
Pfam; PF00047; Ig; 4.
SMART; SM00407; IGc1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hood L.;
"Two mRNAs can be produced alternative RNA processing Cell 20:313-319(1980).
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                        EMBL; V00821; CAA24202.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rogers J.,
Wall R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 433-476 FROM N.A. MEDLINE=80222874; PubMed=6771020;
                                                                                                                                                                                     Alternative
                                                                                                                                                                                                                                                                                   HSSP; P01857; 1FC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            forms of immunoglobulin mu Cell 20:303-312(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 410-476 FROM N.A. (MY MEDLINE=80222873; Pubmed=6771019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Early P., Rogers J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Two mRNAs with different 3' ends encode membrane-bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event-Alternative splicing; Named isoforms=2;
Comment=During differentiation, B lymphocytes
expression of isoform Membrane-bound to isofor
                                                                                                                                                                                                                                                                                                                                                                                                                              MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=P01872-1; Sequence=External; MISCELLANEOUS: The sequence of residues 1-409 is assumed to bidentical with the corresponding region of the secreted form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Secreted;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Membrane-bound;
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 Chordata;
Rodentia;
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19 epsilon chain C r
                                  Honjo T.;
Submitted
SEQUENCE OF 34-421 FROM MEDLINE=83117774; PubMed
                                                                                MEDIINE=84236092; PubMed=6329728; Ishida N., Ueda S., Hayashida H., Miyata T., "The nucleotide sequence of the mouse immuno: comparison with the human epsilon gene seque: EMBO J. 1:1117-1123(1982).
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                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                 NCBI_TaxID=10090;
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                                   PS50835; IG_LIKE; 4. PS00290; IG_MHC; 3.
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P01872;
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Hood L.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE (MYELOMA PROTEIN MOPC 104E).

MEDLINE=79223904; PubMed=111247;

MEDLY M.R., Sibley C.H., Fuhrman J.S., Schilling J.W., Hoo Kehry M.R., Sibley C.H., Fuhrman J.S., Schilling J.W., Hoo "Amino acid sequence of a mouse immunoglobulin mu chain.";

Proc. Natl. Acad. Sci. U.S.A. 76:2932-2936(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Auffray C., Rougeon F.; "Nucleotide sequence of chain of mouse immunoglo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goldberg G.I., Vanin E.F., Zrolka A.M., "Sequence of the gene for the constant Balb/c mouse immunoglobulin.";
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10-OCT-2003 (Rel. 42, Last and
Ig mu chain C region secreted
Mus musculus (Mouse).
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MEDLINE=83075344; PubMed=6816276;
Kehry M.R., Fuhrman J.S., Schilling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (MYELOMA TEPC183)
MEDLINE=81165562; PubMed=6260591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kawakami T., Takahashi N., Honjo T.; "Complete nucleotide sequence of mouse comparison with other immunoglobulin he Nucleic Acids Res. 8:3933-3945(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                    Biochemistry
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Goldberg G.I., Vanin E.F., Zrolka
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                                                                                                                                                                                                                                                                                                           mplete amino acid sequence of a mouse vy chain constant region domains."; chemistry 21:5415-5424(1982).
SUBCELLULAR LOCATION: Secreted (Proba ALTERNATIVE PRODUCTS:
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Takahashi N., Honjo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quence of a cloned immunoglobulin.";
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                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                   chain cDNA from B cells and mouse-human hybridomas.";

Proc. Natl. Acad. Sci. U.S.A. 77:6027-6031(898).

-I- MISCELLANEOUS: All 4 combinations of the S/G and V/G polymorphisms at positions 192 and 216 have been observed in human mu chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-75059123; PubMed=4803843; MEDLINE-75059123; PubMed=4803843; Mertram J., Hilschmann N.; Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.; "The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal.), II: the amino acid sequence of the H-chain type), subgroup H III. Architecture of the complete IgM-molecule.' Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
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P01871;
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MEDLINE=81066716; PubMed=6777162;
Mihaesco E., Barnikol-Watanabe S.,
Hilschmann N.;
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European Bioinformatics Institute. The by non-profit institutions as long
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                                                                                              SVTISWTRQNGEAVKTHTNISESHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSP
                                                                                                               EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
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                   PEKYVTSAPMPEPQAPGRYFAHSILTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKST
                                    ENNYKTTPPVLD--SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
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Pred. No. 6.8e-16;
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/FTId=VAR_003903.
V -> G (in dbSNP:12365).
/FTId=VAR_003904.
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                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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21-JUL-1986 (Rel. 01, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
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P01854;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-40; 68-114 AND 427-
MEDLINE=83065234; PubMed=6815656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bennich H.H., Johansson S.G.O., von Bahr-Lir
(In) Bach M.K. (eds.);
Immediate hypersensitivity: modern concepts
Marcel Dekker, New York (1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE=84207910; PubMed=6327276;
Ueda S., Nakai S., Nishida Y., Hisajima H.,
"Long terminal repeat-like elements flank a
epsilon pseudogene that lacks introns.";
EMBO J. 1:1539-1544(1982).
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Seno M., Kurokawa T., Ono Y., Onda H., Sasada R., Igarashi K.,
Kikuchi M., Sugino Y., Nishida Y., Honjo T.;
"Molecular cloning and nucleotide sequencing of human immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                  Padlan E.A., Davies D.R.;
"A model of the Fc of immunoglobulin E.";
                                                                                                                                                                                                                                                                                                               MEDLINE=87089848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY SEQUENCE (MYELOMA PROTEIN ND)
Bennich H.H., Johansson S.G.O., von Bahr-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The sequence of a human immunoglobulin epsilon heavy chain constant region gene, and evidence for three non-allelic genes."; EMBO J. 1:655-660(1982).
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"Duplication and deletion in the human immunoglobulin epsilon genes.";
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MEDLINE=83001945; PubMed=6288268;
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                                                                                                                                                                                                . Immunol. 23:1063-1075(1986).
SIMILARITY: Contains 4 immunoglobulin-like domains.
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Res. 11:719-726(1983).
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requires a license agreement

(See http://www.isb-sib.ch/announce,

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InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; 1g; 4.
SMART; SM00407; IGcl; 4.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 3.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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MIM; 147180; -.
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RESULT 39
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AC P04221;
DT 20-MAR-1987 (Rel. 04, Created)
DT 10-OCT-2003 (Rel. 20, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig mu chain C region membrane-bound form.
OS Oryctolagus cuniculus (Rabbit).
OC Makaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI TaxID=9986;
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Pred. No. 6.7e-16;
9; Mismatches 155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. The state are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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SMART; SM00407; IGc1; 2.
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InterPro; IPR003597; Ig_cl.
InterPro; IPR00306; Ig_MHC.
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Comment=During differentiation, B lymphocytes
expression of isoform Membrane-bound to isofor
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                   NKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVEPKSCDKTHTC
                                        GSGTRKSRLICOATGFSPKQISVSWLRDGQKVESGVLTKPVEAETKGAGPATFSISSMLT
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                                                                                 YMATSQVLVPSKDVLQGTEEYLVCKVQHSNSNRDLRVSFPVDSELPPNVSVFIPPRDSFS
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                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                      Hellman L., Pettersson U., Bennich H.; "Characterization and molecular cloning of the mRI (epsilon) chain of rat immunoglobulin E."; Proc. Natl. Acad. Sci. U.S.A. 79:1264-1268(1982).-!- SIMILARITY: Contains 4 immunoglobulin-like do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE-83182019; PubMed-6820340;
Kindsvogel W.R., Reddy E.P., Moore J.M., Faust C.
"A cloned cDNA probe for rat immunoglobulin epsil
construction, identification, and DNA sequence.";
  InterPro; IPR007110;
InterPro; IPR003597;
InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 205-306 FROM N.A. MEDLINE=82174576; PubMed=6803238;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA 1:335-343(1982).
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                                                                                A93442; EHRT
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Sciurognathi;
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CONFLICT 168

CONFLICT 308

SEQUENCE 429 J
                                                                                           SEQUENCE FROM N.A.

MEDLINE-85297761; PubMed=2994005;

McGuire K.L., Duncan W.R., Tucker P.W.;

"Phylogenetic conservation of immunoglobulin comparison of hamster and mouse Cmu genes.";

Nucleic Acids Res. 13:5611-5628(1985).
                                                                                                                                                                                                      01-JAN-1988 (Rel. 06, Created)
01-FEB-1996 (Rel. 33, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
Ig mu chain C region.
Mesocricetus auratus (Golden hamster).
Eukaryota, Metazoa, Chordata, Craniata
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PROSITE; PS50835; IG_LIKE;

PROSITE; PS00290; IG_MHC; :

Immunoglobulin domain; Immu
                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                                                                                                                              Mesocricetus.
NCBI_TaxID=10036;
[1]
                                                                                                                                                                                              Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                            416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324 KNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGM--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101;
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                                                                                                                                                                                                                                                                                                                                           973
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                              non-profit institutions as long and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                    PIVRSITKAPGKRSAPEVYVFLPPEEEE--KDKRTLTCLIQNFFPEDISVQWLQDSKLIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YCFVYGHIQNDVSIHW--LMDDRKIYETHAQNVLIKEEGKLASTYSRLNITQQQWMSEST
                                                                                                                                                                                                                                                                                                                                                                                                                                               PIEKTISKAKGOPREPQVYT-LPPSRDELTKNQVSLTCLVKGFYPSDIAVEW--ESNGOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -NITVTWVRERKKSIGSASQRSTKHHNATTSITSILPVDAKDWIEGEGYQCRVDHPHFPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FTCKVTSQGENYWAHTRRCSDDE-PRGVITYLIPPSPLD-LYENGTPKLTCLVLDLESEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTCP--
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                                                                                                                                                                                                                                                                                                                                                                                        KSQHSTTTP
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305
414
168
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.4%;
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R -> N (
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Pred. No. 1.1e-15;
9; Mismatches 114;
                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -> N (IN REF. 2).
-> L (IN REF. 2).
D2970B34EF8A72B0
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                  noved. Usage by and for (See http://www.isb-sib.
                                                                                                                                                                                                                                         update)
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                           as its content in
                                                                                                                   heavy chains:
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                                                he EMBL outstation restrictions on it
is ...
and for commerc.
~sib.ch/announce/
                                                             a collaboration -
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an
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394
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                                                                                                                                                                                                                                                                                           Similarity
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PS50835; IG_LIKE; 4.
PS00290; IG_MHC; 3.
                                TLPPSRDEL-TKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGS--F
| :|::| : ::||||||| | :| | :| | :| :: |
QQPLAREQLILRESATVTCLVKGFSPADIFVQWLQRGQPLSQDKYVTSAPWREPQAPHLY
                                                                               QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE-----PQVY
                                                                                                     A-----PIPPSFVGIFLNKSATLTCLVTNLATYD-TLNISWSSRSGEPLETKIKLTES
                                                                                                                                                 ------LPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQKN----
                                                                                                                                                                                                                                               FPLVSCESPLSDENLVAMGCLARDFLPSSISFSW---NYQNKSEVNQGVRTFPTLRMGEK
                                                                                                                       GGPSVFLFPPKPKDT-LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                           VPSRDAFSGPAPRKSRLFCEASNFSPKQITVSWLRDGKPVKSGFTTEPV---TPE----
                                                                                                                                                                                                              YAATSQVFLP----
                                                                                                                                                                                                                                                                FPLA----FTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKK
FTHSVLTVTEEEWNSGETYTCVVGHEALPHMVTERTVDRSTG
                FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                    HPNGTFSAIGEANVCVEDWDSGKEFVCTVTHRDLPSPQKKFISK---
                                                                                                                                        ---- DRGSGPRTYKVISTLTITESDWLNLSVYTCRVDHRGLTFWKNVSSTCAASPSTDIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR007110; Ig-like.
IPR003597; Ig_cl.
IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              email to license@isb-sib
                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain;
                                                                                                                                                                                                                                                                                                                 10.4%;
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CH2.
CH3.
CH3.
CH4.
INTERCHAIN (WITH I
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (WITH I
BY SIMILARITY.
                                                                                                                                                                                                                                                                                Score 355.5; |
Pred. No. 1.2e
32; Mismatches
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N-LINKED
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BY SIMILARITY
INTERCHAIN (WITH HEAVY
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435
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RESULT 43
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Matches 84
MUC_RABIT
P03988;
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig c1.
InterPro; IPR00306; Ig_MHC.
Pfam; PF00047; Ig; 3.
SMART; SM00407; IGc1; 2.
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GO; GO
GO; GO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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Hoppe-Seyler's Z. Pl
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAR-1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
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-OCT-2001 (Rel. 40, Last annotation updat
mu heavy chain disease protein (BOT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO:0005624; C:membrane fraction; NAS. GO:0003823; F:antigen binding; TAS. GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primary structure of mu-chain-unserver primary structure of mu-chain-unserver positions."; no-acid sequence of the N-terminal 42 positions."; no-acid sequence of mu-chain 36:105-118(1994).
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                                                                                                                      SPEKYVTSAPMPEPQAPGRYFAHSILTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKS
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                                                                                                                                                                                                                                                                                           WSTPVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
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                                                                                                                                                                                                                                                                                                                                        GPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNIKVL--PT
                                                                                                                                            -ENNYKTTPPVLD--SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
                                                                                                                                                                    PLKQTISRPKGVALHRPDVYLLPPAREQLNLRESATITCLV
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                                                                                                                                                                                                                    -SVTISWTRQDGEAVKTHTNISESHPNATFSAVGEASICEDDWDSGERFTCTVTHTDLPS
                                                                                                                                                                                                                                                                                                                                                                                                                391 AA;
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43
156
262
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1 42 PRE-C-PART
43 155 CH3.
56 261 CH3.
            STANDARD;
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S., Mihaesco E.,
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                                                                                                                                                                                                                                                                                                                                                                 61;
                                                                                                                                                                                                                                                                                                                                                                Score 353.5; I
Pred. No. 1.3e-
51; Mismatches
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CH2.
CH3.
CH4.
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(NO V REGION HOMOLOGY)
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Best Local
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23-OCT-1986 (Rel. 02, Last sequence update)
23-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
1g mu chain C region secreted form.
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                 CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                 DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bernstein K.E., Alexander C.B., Reddy E.P., Northwest Sequence of a cloned cDNA encoding of VHa2 allotype: comparisons with VHa1 and n J. Immunol. 132:490-495(1984).
                                                                                                                                                                                                                                                                                                                               SMART; SM00407; IGc1; 2.

PROSITE; PS50835; IG LIKE; 4.

PROSITE; PS500290; IG_MHC; 3.

Immunoglobulin domain; Immunoglobulin
Alternative splicing.
                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; K01357; -; 1
PIR; A02164; MHRB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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InterPro; IPR003597;
InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP;
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ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Secreted;
IsoId=P03988-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Membrane-bound
IsoId=P04221-1; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2;
Comment=During differentiation, B lymphocyt
expression of isoform Membrane-bound to iso
                       223
                                             116;
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 9
                                                        Similarity
YPLVSCEGALTDGNLVAMGCLARDFLPSSVTFSW-SFK-NNSEISSRTVRTFPVVKRGDK
                      FPL----AFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKK
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OC ELKAT
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                                                                                                 InterPro; IPRO07110; Ig-1ike.
InterPro; IPRO03597; Ig_c1.
InterPro; IPRO0306; Ig_MHC.
Pfam; PF00047; Ig; 4.
SMART; SM00407; IGc1; 3.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_MHC; 3.
     Immunoglobulin (
NON TER 1
DOMAIN 1
DOMAIN 106
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01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ig mu Chain C region.
Ig mu Chain C region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-89232144; PubMed-2497033; Ishiguro H., Ichihara Y., Namikawa T., Nagatsu T., Kurosawa Y.; "Nucleotide sequence of Suncus murinus immunoglobulin mu gene and comparison with mouse and human mu genes."; FEBS Lett. 247:317-322(1989).
                                                                                                                                                                                                                                                              EMBL; X13920; CAA32113.1; ALT_INIT.
PIR; S03961; S03961.
HSSP; P01842; 7FAB.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suncus murinus (House shrew) (Musk shrew).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutel
Mammaila, Eutheria, Insectivora, Soricidae, Crocidurinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Liver;
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                                                                              domain; Immunoglobulin
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SILTVSEKDWSSGESFSCVVGHEALPLSVTEKAVDKTSG
                               SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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Pred. No. 3.7e-
90; Mismatches
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21-JUL-1986 (Rel. 01, Created)
T 15-JUL-1999 (Rel. 38, Last annotation up a lg mu chain C region.
Canis familiaris (Dog).
Eukaryota: Mor-
                                                                                                              MUC_CANFA
P01874;
21-JUL-1986
21-JUL-1986
15-JUL-1999
                                                                                                                                                                   CANFA
                                                       Calls ramiliaris (Dog).

Bukaryota; Metazoa; Chordata; Craniata; Ve.

Mammalia; Eutheria; Carnivora; Fissipedia;

NCBI TaxID=9615;

[]1
SEQUENCE OF 1-177 (MOO).
MEDLINS=80077682; PubMed=117299;
McCumber L.J., Capra J.D.;
"The complete anino-acid sequence
Mol. Immunol. 16:565-570(1979).
                                                                                                                                                        STANDARD;
          of.
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          canine
                                                                       Vertebrata;
ia; Canidae;
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           큺
          chain.
                                                                       Euteleostomi;
Canis.
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ID ALC_RA
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Best Local S
Matches 100
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P01879;
21-JUL-1986 (Rel. 01, 0
21-JUL-1986 (Rel. 01, 1
15-MAR-2004 (Rel. 43, 1
    cDNA encoding
Nucleic Acids |
-!- FUNCTION:
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SEQUENCE
                     SEQUENCE FROM N.A.

MEDILINE-84144059; PubMed-6322114;

Knight K.L., Martens C.L., Stoklosa C.M., Sch

"Genes encoding alpha-heavy chains of rabbit

CDNA encoding IgA-g subclass alpha-chains.";

Nucleic Acids Res. 12:1657-1670(1984).
                                                                                                                                                                                 Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                  NCBI_TaxID=9986;
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NON_TER
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SMART; SM00407; 1Gc1; 2. .
PROSITE; PS50835; IG_LIKE; 4. .
PROSITE; PS00290; IG_MHC; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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Wasserman R.L., Capra J.D.;
"Amino acid sequence of the Fc region of a
interspecies homology for the IgM class.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P01857;
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                                                                                                                                                                                                                                                    alpha chain C region (Fragment).
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                                                                                                                                                                                                                                                                                                                                                            STANDARD;
    alpha
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    the major
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Pred. No. 1.2e-
76; Mismatches
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    immunoglobulin class
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..2e-14;
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MUC_CHICK
PUC_TS:
21-JUL-1986
01-FEB-1991
15-JUL-1999
                                                                                             15-JUL-1999 ....
Ig mu Chain C region.
Ig allus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; C
                                                                                    Gallus.
SEQUENCE OF 80-446 FROM N.A. MEDLINE=83299221; PubMed=6310496;
                                                              NCBI_TaxID=9031;
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(Rel. 01, Created) (Rel. 17, Last sec (Rel. 38, Last and

sequence update) annotation updat

update)

Craniata; Vertebrata; ; Galliformes; Phasiani

Phasianidae;

Euteleostomi;

STANDARD;

446

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Query Match
Best Local S
Matches 85
                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003006; Ig_MHC.

Pfam; PF00047; ig; 2.

SMART; SM00407; IGc1; 2.

PROSITE; PS00395; IG_LIKE; 2.

PROSITE; PS00290; IG_MHC; 2.

Immunoglobulin domain; Immunoglobulin C region; Repeat.

NON_TER 1 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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HSSP; P01857; 1FC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunologic system.
MISCELLANEOUS: This immunoglobulin belongs to the I
MISCELLANEOUS: This immunoglobulin belongs to the I
It was isolated from a rabbit homozygous FOR A2, N8
F71, G75 heavy chain haplotype.
SIMILARITY: Contains 2 immunoglobulin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                secretions. It may ser
and to prevent access
immunologic system.
                              597
                                                            192
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 252
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                                                                                                                                                                                                                                                                                                         l Similarity
85; Conserv
                                                                            VSLTCLVKGFYPSDIAVEWESNGQ--PENNY---KTTPPVLDSDGSFFLYSKLTVDKSRW
                                                                                                                       VLPSSAETWKARTEFTCTVTHPEIDSGSLTATISRGVVTP--PQVHLLPPPSEELALNEQ
NQGDTYSCMVGHEGLAEHFTQKTIDRLAG
                              QQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                          VTLTCLVRGFSPKDVLVSWRHQGQEVPEDSFLVWKSMPESSQDKATYAITSLLRVPAEDW
                                                                                                                                                    VLTVLHQDWLNGKEYKCKVSNKALPA-PIEKTISKAKGQPREPQVYTLPPSRDELTKN-Q
                                                                                                                                                                                PDLGD-LLLGRDASLTCTLSGLKNPEDAV-FTW--EPTNGNEPVQQRAQRDLSGCYSVSS
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276 II
32256 MW;
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; Ig_cl.
; Ig_MHC.
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                                                                                                                                                                                                                                                                                                        Score 305; DB 1
Pred. No. 1.2e-1
4; Mismatches ]
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InterPro; IPR003006; Ig_MHC.
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SMART; SM00407.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dahan A., Reynaud C.-A., Weill J.-C.;
"Nucleotide sequence of the constant
chain immunoglobulin mRNA,";
Nucleic Acids Res. 11:5381-5389(1983)
                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X01613; CAA:
PIR; A02170; MHCH
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; PS50835; IG_LIKE; 4.
; PS00290; IG_MHC; 3.
                                                                                                                    SSIAFTWFDSNNSSVSGMDVI--PKVISG-----PPYRAVSR--IQMNQSEG
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 EMRNTSKRMECGLEPVVQQDI - - - -
                 EPKSCDKTHTC--PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP-E
                                                         AKVSKREKP---VWVLN--PEAGMWQCLLSDSGQVLLESNIKVLPT-WSTPV-----
                                                                                                KLHQEVNLVVMRATQLQKNLTCEVWGP---TSPK---LMLSLKLENKE-----
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C-TERMINAL
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INTERCHAIN (WITH )
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-LINKED (GLCNAC.
3CB0CE108949BD17
                                                                                                                                                          Mismatches
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No. 5.
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(GLCNAC...
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01-NOV-1991 (Rel. 20, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
19 heavy chain C region (Clone 12022) (Fragment).
Heterodontus francisci (Horn shark).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes
Elasmobranchii; Galeomorphii; Heterodontoidea; Heterodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=88328985; PubMed=3138109;
Kokubu F., Hinds K., Litman R., Shamblott M.J., Litman G.W.;
"Complete structure and organization of immunoglobulin heavy chain constant region genes in a phylogenetically primitive vertebrate.";
EMBO J. 7:1979-1988(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig;
SMART; SM00407; IG
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01-NOV-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heterodontidae; Heterodontus.
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PS50835; IG_LIKE;
PS00290; IG_MHC;
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IPR003597; Ig_c1.
IPR003006; Ig_MHC.
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IG-LIKE 3.
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N-LINKED (CON-LINKED CON-LINKED C
                            Score 297;
Pred. No. 6.
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01-NOV-1991 (Rel. 20, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain C region, membrane-bound form (Clone Heterodontus francisci (Horn shark).
Elasmobranchii; Galeomorphii; Heterodontoidea; Heterodon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentitles requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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p15 heavy chain C region, secreted form (Clone Heterodontus francisci (Horn shark).
        MEDLINE=88328985; PubMed=3138109; Kokubu F., Hinds K., Litman R., Shamblott M. "Complete structure and organization of immu constant region genes in a phylogenetically EMBO J. 7:1979-1988(1988).
                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmobranchii; Galeomorphii; Heterodontoidea; Heterodontiformes; Heterodontidae; Heterodontus.
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Pred. No. 9.4e-12;
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SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL

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Query Match
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Matches 117
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InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 4.
SMART; SM00407; IGC1; 2.
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PROSITE; PS00290; IG_MHC; 3.
Immunoglobulin_domain; Immunoglobulin
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PIR; S01853; HVRKCS.
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                                                                                                                       TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQV-YTLPPSRD
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AEEWASGASYSCVVGHEAIPLKIINRTVNKSSG
                      KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                     ELTKNOVSLTCLVKGFYPSDIAVEWESNGQPEN--NYKTTPPVLDSD-GSFFLYSKLTVD
                                                                                                ADSVISTVNISTQAWLSGAEFYCVVNHQDLPTPLRASIHKEEVKDLREPSVSILLSPAED
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                                                                                                                                                                                                                                                                                                                                                     TSVSWKKDNEPITTGLKTYPSVLNKKGTYTQSSQLTITESEVGSSKIYCEVRRGES--VW
                                               VSAORFLSLTCLVRGFFPREIFVKWTVNDKSVNPGNYKNTEVMAENDNSSYFIYSLLSIA
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Pred. No. 1.1e
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L.le-11;
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                                                                                                MIM; 147000; -.
GO; GO:0005624; C:membrane fraction; NA
GO; GO:0003823; F:antigen binding; TAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_C1.
InterPro; IPR0031006; Ig_MHC.
                                                                                                                                                                                                              HSSP; P01810; 2FBJ.
Genew; HGNC:5479; IGHA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Torano A., Putnam F.W.; "Complete amino acid sequence of the alpha 2 heavy IGA2 immunoglobulin of the A2m (2) allotype."; Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
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01-FEB-1991 (Rel. 17,
15-MAR-2004 (Rel. 43,
Immunoglobulin domain; Immunoglobulin C
NON_TER 1 1
DOMAIN 6 98 IG-LIKE 1.
                                            Pfam; PF00047; ig; 3. SMART; SM00407; IGcl; 2. SMART; PS50835; IG_LIKE; 3 PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                            EMBL; J00221; AAB59396.1;
PIR; B22360; B22360.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                molecule.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=79180140; PubMed=286295;
Tsuzukida Y., Wang C.-C., Putnam F
"Structure of the A2m(1) allotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE (MYELOMA PROTEIN LAN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Flanagan J.G., Léfranc M.-P., Rabbitts T.H.; mechanisms of divergence and convergence of the human immunoglobulin alpha 1 and alpha 2 constant region gene sequences."; Cell 36:681-688(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91054387; PubMed=2241915;
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IGHA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The
                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: Monomeric or polymeric.
MISCELLANEOUS: The sequence of the A2m(1) allotype is shown.
SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Ig alpha is the major immunoglobulin class in body secretions. It may serve both to defend against local infection and to prevent access of foreign antigens to the general
                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunologic system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       structure and function of human IgA.";
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F.W.;
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                              region; Glycoprotein; Repeat.
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D HVC3 HETFR

C P230B6;
C P230B6;
T 01-NOV-1991 (Rel. 20, Created)
T 01-NOV-1991 (Rel. 20, Last sequence update)
T 10-CCT-2003 (Rel. 42, Last annotation update)
E 19 heavy chain C region (Clone 6121) (Fragment).
S Heterodontus francisci (Horn shark).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chc Elasmobranchii; Galeomorphii; Heterodontoidea; Heterodontus.

K NCBI_TaxID=7792;
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                                                                                                                                                                                                                                                                                                        VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HPRLSLHRPALEDLLLGSEANLTCTLTGL-RDASGATFTWTPSSGK--SAVQGPPERDLC
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P -> S (IN A2M(2))
/FTId=VAR 003879.
P -> R (IN A2M(2))
/FTId=VAR 003880.
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/FTId=VAR 003881.

D -> E (IN A2M(2)

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V -> I (IN A2M(2)
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Pred. No. 4e
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IG-LIKE 3.
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V -> A (IN A2M(2)
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                                          Heterodontiformes;
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Best Local Sim
Matches 116;
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InterPro; IPR003597;
InterPro; IPR003006;
Pfam; PF00047; 19; 3.
SMART; SM00407; IGC1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          constant
EMBO J. 7
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00407; IGc1; 2. PROSITE; PS50835; IG_LIKE; PROSITE; PS00290; IG_MHC; 3
                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X07782; CAA30615.1; -. PIR; S01852; HVRKC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kokubu F., Hinds K., Litman R., Shamblott M.J., Litman G.W.,
"Complete structure and organization of immunoglobulin heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Spleen;
MEDLINE=88328985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                   187
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                                                                                                                                                                                                                                                                                                                      Similarity 26. 
16; Conservative
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DIAVEWESNGQPEN--NYKTTPPVLDSD-GSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL
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                                                  EYKCKVSNKALPAPIEKTISKAKGQP-REPQV-YTLPPSRDELTKNQVSLTCLVKGFYPS
                                                                                    TLNCI--
                                                                                                          EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK 496
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                                                                                                                                                                                                    MRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSG
                                                                                                                                                                                                                           K---GDKVHPTVILTQSSSEEITSRRFATVLCSIIDFHPESITVSWLKDGQ-HMESGFVT
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                                                                                                                                                                                                                                                                          VLNKKGTYTO-
                                                                                                                                                                                                                                                                                                VYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSVKRVTQDP
                                     EFYCVVNHQDLPTPLRASIHKEEVKDLREPSVSILLSPAEDVSAQRFLSLTCLVRGFSPR
                                                                                                                                -VTQSRNI------TGSQVPCSCND----PVIKLLPPSIEQVL-LEATV
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                                                                                 - VSNAPYGVNVSW---TQEQKSLKSEIAVQPGEDADSVISTVNISTQAWLSGA
                                                                                                                                                                               SPTCGVNGTFSATSRLT-----VPARE---WFTNK---VYTCQVSHQG
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; Ig_cl.
; Ig_MHC.
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IG-LIKE 2
IG-LIKE 3
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                                                                                                                                                                                                                                                                                                                    Score 281.5; DB 1;
Pred. No. 5.6e-11;
3; Mismatches 164;
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MBL outstation -
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This SWISS-PROT entry is copyright. It is produced through a collar between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commentities requires a license agreement (See http://www.i.c.
                                                                                                                                                                                                                                                                                 characterization (
Hoppe-Seyler's Z.
[5]
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ALC1 HU
P01876;
                                                                                                                                                                                                 Biochem.
                                                                                                                                                                                                                                                                                         MEDIINE-80114124; PubMed-393607;
Yang C.-Y., Kratzin H., Gotz H., Hilschmann N.;
"Rule of antibody structure. Primary structure of a human monoclonal
IgA-immunoglobulin (myeloma protein Tro). VII. Purification and
characterization of the disulfide bridges.";
Hoppe-Seyler's Z. Physiol. Chem. 360:1919-1940(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE=84130179; PubMed=6421489;

Flanagan J.G., Lefranc M.-P., Rabbitts T.H.;

Flanagan of divergence and convergence of the human alpha 1 and alpha 2 constant region gene sequences.";

Cell 36:681-688(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986
01-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Putnam F.W., Liu Y.-S.V., Low T.L.K.;
"Primary structure of a human IgAl immunoglobulin.
IgAl protease, digestion, Fab and Fc fragments, and
amino acid sequence of the alpha 1 heavy chain.";
                                                                                                                                                                                                                                                                                                                                                                                   DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                            "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro.), II. The amino acid sequence of the H-chain, alpha-type, subgroup III; structure of the complete IgA-molecule."; Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kratzin H., Al
Hiləchmann N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE (MYELOMA PROTEIN TRO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                          Kerr M
                                                                                                                                                                                                                                                      MEDLINE=91054387; PubMed=2241915;
                                                                                                                                                                                                                                                                      REVIEW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=79151016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE (MYELOMA PROTEIN
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alpha-1 chain C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B101.
                                                                                                                         immunologic system.
SUBUNIT: Monomeric or polymeric
SIMILARITY: Contains 3 immunogle
                                                                                                                                                                   FUNCTION: Ig alpha is the major immunoglobulin class in body secretions. It may serve both to defend against local infection and to prevent access of foreign antigens to the general
                                                                                                                                                                                                                          structure and function of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUMAN
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P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Altevogt P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 01, Created)
(Rel. 17, Last sec
(Rel. 43, Last ann
                                                                                                                                                                                                               271:285-296(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254:2865-2874(1979).
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Primates;
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                          (See http://www.isb-sib.ch/announce,
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Best Local &
Matches 93
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InterPro; IPRO03597; Ig_cl.
InterPro; IPRO03597; Ig_cl.
InterPro; IPRO03006; Ig_MHC.
Pfam; PF00047; ig; 3.
SMART; SM00407; IGcl; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00200; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C
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GO; GO:0003823; F:antigen binding; NAS
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PIR; A22360; A1HU.
PDB; 1IGA; 15-JUN-99.
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                     VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG--SFFLYSKLTVDKSRW
                                                      SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-
||| : | : || : || : || : || : || : ||
                                                                                  RPALED-LILGSEANLTCTLTGL-RDASGVTFTWTPSSGK--SAVQGPPERDLCGCYSVS
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VTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRVAAEDW
                                                                                                        PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV
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E -> D (in dbSNP:1407).
FTId=VAR_014602.
TPS -> PST (IN REF. 2).
E -> B (IN REF. 3).
P -> S (IN REF. 3).
P -> R (IN REF. 3).
H -> R (IN REF. 3).
-> E (IN REF. 3).
-> E (IN REF. 3).
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IG-LIKE 2.
IG-LIKE 3.
INTERCHAIN
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Pred. No. 5.6e-11
9; Mismatches 13
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OR 123-182
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DOMAIN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50835; IG_LIKE; 3. PROSITE; PS00290; IG_MHC; 1. Immunoglobulin domain; Immuno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 3. SMART; SM00407; IGc1; 2.
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HSSP; P01810; 2FBJ.
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01-FEB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation updat
Ig alpha-1 chain C region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9595;
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \text{Awamura S., Omoto K., Ueda S.;}
\text{Nucleotide sequence of the gorilla immunoglobulin alpha}
\text{Vucleic Acids Res. 17:6732-6732(1989).}
\text{Indextall the content of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Buropean Bioinformatics Institute. The by non-profit institutions as long if the by non-profit institutions as required and this statement is not removed. Ities requires a license agreement (See leand an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Ig alpha is the major immunoglobulin class secretions. It may serve both to defend against local and to prevent access of foreign antigens to the generations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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278; DB 1;
No. 8.1e-11;
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                                                                                   LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG------LQLDETC
                                                                                                                PPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFA
                                                                                                                                                                          PERDLCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKS-GNMFRPEVHLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE=88328985; PubMed=3138109;
Kokubu F., Hinds K., Litman R., Shamblott M.J., Litman G.W.;
"Complete structure and organization of immunoglobulin heavy chain constant region genes in a phylogenetically primitive vertebrate.";
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10-OCT-2003 (Rel. 42, Last annotation update)
19 heavy chain C region (Clone 6125) (Fragment).
Heterodontus francisci (Horn shark).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthye Elasmobranchii; Galeomorphii; Heterodontoidea; Heterodontiformes; Heterodontidae; Heterodontus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           constant region genes in a phylogenetically primitive v EMBO J. 7:1979-1988(1988).
-i- SIMILARITY: Contains 3 immunoglobulin-like domains.
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                                                                                                                         PROSITE; PS50835; IG_LIKE; PROSITE; PS00290; IG_MHC;
                                                                                                                                                                                                     InterPro; IPR007110;
InterPro; IPR003597;
InterPro; IPR003006;
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HSSP; P01857; 1FC1.
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                                                                                                                                                                   SM00407;
                                                                                                       Lobulin
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IG-LIKE 3.
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01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
19 mu chain C region membrane-bound form.
1ctalurus punctatus (Channel catfish)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
1ctaluridae; Ictalurus.
EMBL; X52617; -; NOT_ANNOTATED_CDS.

HSSP; P01857; 1FC1.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
SMART; SM00407; Ig; 3.
SMART; SM00407; IGC1; 1.
PROSITE; PS00835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 2.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it most by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia entitles requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@sib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wilson M.R., Marcuz A., van Ginkel F., Miller N.W., Clem L.W., Middleton D., Warr G.W.;
Middleton D., Warr G.W.;
"The immunoglobulin M heavy chain constant region gene of the chanr catfish, Ictalurus punctatus: an unusual mRNA splice pattern produc the membrane form of the molecule.";
Nucleic Acids Res. 18:5227-5233(1990).
-I- MISCELLANEOUS: During differentiation, B lymphocytes switch fro expression of membrane-bound IgM to secretion of IgM. The mu chains of membrane and secreted IgM differ in their C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=90384824; PubMed=2119496;
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
 Auffray C., Nageotte R., Sikorav J.-L., Heidm: "Mouse immunoglobulin A: nucleotide sequence of the alpha heavy chain derived from cloned
                              SEQUENCE FROM N.A. (MYELOMAS ABE4 MEDLINE=81261947; PubMed=6790349;
                                                                                              Mus musculus (Mouse)
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                                                                         Craniata; Vertebrata; |
Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Robinson E.A., Appella E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-254 AND 291-344 (M511).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
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"Amino acid sequence of a mouse myeloma immunoglobin heavy chain (MOPC 47 A) with a 100-residue deletion.";
J. Biol. Chem. 254:11418-11430(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=80049769; PubMed=115869;
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Complete amino acid sequence of a mouse immunoglobulin alpha chain
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MISCELLANEOUS: M511 sequence was compared with that of mouse MOPC 47A, and a genetic mechanism for the deletion of the CH3 domain of the mutant chain is proposed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Ig alpha is the major immunoglobulin class in body secretions. It may serve both to defend against local infection and to prevent access of foreign antigens to the general
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISCELLANEOUS: The final C-region domain is deleted from Ref. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pean Bioinformatics Institute. There are no restrictions non-profit institutions as long as its content is in and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS50835; IG_LIKE; 3. PS00290; IG_MHC; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                region; Glycoprotein; Repeat
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SEQUENCE
Ohnishi H., Kubota M., San "BIT (Bit) maps to mouse c Genomics 40:504-506(1997).
                                                                                                                                                                                                                                                                   Fujioka Y., Matozaki T., Amano K., Matsuda Y. Fujioka Y., Kasuga M.;
"Mouse and human SHPS-1: molecular cloning localization of genes.";
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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P97797; O08907;
Q9WTN4;
                                                                                         STRAIN=BALB/c; TISSUE=Brain;
MEDLINE=97230468; PubMed=9073522;
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                                                      Kubota M., Sano S.-I.
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ASN-224.
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                                                                                                                                                                                      VARIANTS ALA-29; ARG-67; ARG-91;
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STRAIN-C57BL/6; TISSUE-Fetal thymus;
MEDLINE-98380500; PubMed-9712903;
Veillette A. Thibaudeau E. Latour S.;
"High expression of inhibitory receptor with protein tyrosine phosphatase SHP-1
J. Biol. Chem. 273:22719-22728(1998).
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STRAIN-BALB/C; TISSUE-Brain, and Cerebellum; MEDLINE-98012243; PubMed-9348339; Comu S., Weng W., Olinsky S., Ishwad P., Mi Z., Hempel J.
                                                                                                                                                                                                              N-GLYCOSYLATION, PHOSPHORYLATION BY JAK? HORMONE, AND INTERACTIONS WITH JAK2 AND MEDLINE=98175985; PubMed=9507023; Stofega M.R., Wang H., Ullrich A., Carte "Growth hormone regulation of SIRP and and association.";
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                                                           [10]
INTERACTION WITH CD47, AND TISSUE CMEDLINE-99091586; PubMed-9872987;
MEDLINE-99091586; PubMed-9872987;
MEDLINE-99091586; PubMed-9872987;
MEDLINE-99091586; PubMed-9872987;
MEDLINE-199091586; PubMed-9872987;
MEDLINE-199097; PubMed-9872987;
MEDLINE-199097; PubMed-9872987; PubMed-9872987; PubMed-9872987; PubMed-9872987; PubMed-9872987; PubMed-9872987; PubMed-9872987; PubMed-9872987; PubMed-9872987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION, TISSUE SPECIFICITY, AND MEDLINE=90152134; PubMed=2303162; Chuang W., Lagenaur C.F.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Gene structure of mouse BIT/SHPS-1."; Blochem. J. 344:667-675(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                         neurite outgrowth.";
Dev. Biol. 137:219-232(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang H., Chen Z., Ullrich A.; "Epidermal growth factor-induced association of SHP2 with mouse
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MEDLINE-21363810; PubMed-11471062;
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                                                  "Integrin-associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Central nervous system antigen
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                                                                                                                                                                                     Biol.
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274:559-562 (1999)
                                                                                                                                                                                     273:7112-7117(1998)
                                                                                                                                  AND TISSUE SPECIFICITY
                                                  is a ligand for the P84 neural adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND DEVELOPMENTAL STAGE
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and SHP-2
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EMBL; D87967; BAA13520.1; -.
EMBL; D87968; BAA2376.1; -.
EMBL; D857968; BAA20376.1; -.
EMBL; D857964; AAB92591.1; -.
EMBL; AF072543; AAC2488.1; -.
EMBL; AF072544; AAC24887.1; -.
EMBL; AB024507; BAA89290.1; JOINI
EMBL; AB024507; BAA89290.1; JOINI
EMBL; AB024501; BAA89290.1; JOINI
EMBL; AB024502; BAA89290.1; JOINI
EMBL; AB024503; BAA89290.1; JOINI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=3; Synonyms=b, Small;
IsoId=P97797-3; Sequence=VSP_007031;
IsoId=P97797-3; Sequence=VSP_007031;
spinal cord, cerebellum and spleen, and at much lower levels in kidney, thymus, heart, lung and liver. Within the cerebellum, highly expressed throughout the molecular layer, and in synaptic glomeruli in the granule cell layer. Detected in neurons of the hippocampus and dentate gyrus, and in olfactory bulb. Not detected in Purkinje cells. Highly expressed in the plexiform layers, optic fiber layer and the outer segments of the photoreceptor layer in the retina. Highly expressed in macrophages. Isoform 3 is detected at very low levels in all tissues tested.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as docking protein and induces translocation of PTPN6,
PTPN11 and other binding partners from the cytosol to the
plasma membrane. Supports adhesion of cerebellar neurons, neurite
outgrowth and glial cell attachment. May play a key role in
intracellular signaling during synaptogenesis and in synaptic
function. Involved in the negative regulation of receptor tyrosine
kinase-coupled cellular responses induced by cell adhesion, growth
factors or insulin. Mediates negative regulation of phagocytosis,
mast cell activation and dendritic cell activation. CD47 binding
prevents maturation of immature dendritic cells (By similarity).
-!- SUBUNIT: Binds PTPN11 when tyrosine-phosphorylated, except in
macrophages, where it primarily binds PTPN6. Binds GRB2 vitro.
Binds FGR. Binds JAK2 irrespective of its phosphorylation status
and forms a stable complex. Binds SCAP1 and/or SCAP2. The
resulting complex recruits FYB. Binds PTK2B (By similarity).
-!- SUBCELIULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collat between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con entities requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Negative regulation of phagocytosis in
kinase family member, Fgr.";
J. Exp. Med. 19::515-528(2000).
-1- FUNCTION: Immunoglobulin-like cell s
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Lowell C.A., Lagenaur C.F.
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INTERACTION WITH FGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              day 7 to 17.
PTM: N-glycosylated.
PTM: N-glycosylated on tyrosine residues.
PTM: Phosphorylated on tyrosine residues.
SIMILARITY: Contains 2 immunoglobulin-like C1-type domains.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=2; Synonyms=a', Large;
IsoId=P97797-2; Sequence=VSP_007032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=1; Synonyms=a; IsoId=P97797-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Comment=Additional isoforms
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Best Local (
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                                                                                                                                   SHS1_BOVIN STANDARD; PRT; 506 AA. 046631; 046632; 10-0CT-2003 (Rel. 42, Created) 10-0CT-2003 (Rel. 42, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
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EMBL;
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EMBL;
SEQUENCE FROM N.A.,
                     NCBI_TaxID=9913;
                                      Mammalia;
Bovidae;
                                                Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                    Protein-tyrosine phosphatase non-receptor type substrate 1 (SHP substrate-1) (SHPS-1) (Inhibitory receptor SHPS-1) (SPS-1) (STP-alpha-1) (MyD-1 antigen) PTPNS1 OR SHPS1 OR STRP OR MYD1.
                                                                                                                                                                                                      BOVIN
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MGI:108563; Ptpns1
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AB018194;

AB024500;

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                                                                                                                                                                                                                                                       YTSLFLVNSSAHREDVVFTCQVKHDQQPAITRNHTVLGLAHSSDQGSMQTFPG
                                    Bovinae;
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                                                                                                                                                                                                                                                                              LYSKLTVDKSRWQQGNVFSCSVMHE---ALHNHYT-
                                                                                                                                                                                                                                                                                                        PTVKVTQQSPTSMNQVNLTCRAERFYPEDLQLIWLENGNVSRN--DTPKNLTKNTDGTYN
                                                                                                                                                                                                                                                                                                                              PS----RDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVL--DSDGSFF 584
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BAA89289.1;
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AAK56107.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brooke G.P., Parsons K.R., Howard C.J.;
"Cloning of two members of the SIRP alpha family of protein tyrosine phosphatase binding proteins in cattle that are expressed on monocyte and a subpopulation of dendritic cells and which mediate binding to CD4 T_cells.";
                                                                                                                                                       CHAIN
                                                                                                                                                                PROSITE; PS50835; IG_LIKE; 3.

PROSITE; PS00290; IG_MHC; FALSE NEG.

Repeat; Signal; Transmembrane; Tmmunoglobuli

Glycoprotein; Phosphorylation; Polymorphism.

SIGNAL 1 29 POTENTIAL.
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STRAIN=Friesian; TISSUE-Peripheral blood;
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                                                                                                                                     DOMAIN
                                                                                                                                                                                                                Pfam; PF00047; ig; 3. SMART; SM00407; IGc1; 2.
                                                                                                                                                                                                                                InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
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 RES
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Y11046; CAA71943.1; -.
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SH2-BINDING
SH3-BINDING
SH3-BINDING
SH2-BINDING
SH2-BINDING
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IG-LIKE
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                               PROTEIN-TYROSINE TYPE SUBSTRATE 1.
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   PHOSPHORYLATION
                                                                              POTENTIAL.
                                                                                      C1-TYPE
                                                                                                          V-TYPE
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(POTENTIAL).
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ITION (BY TYR-KINASES)
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ASN-367; LEU-422;
                                                                                                                                                                                    domain;
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 QTSWFLVNSSAHREAVVLTCQVEHDG-----QPAVSKNHTLEVSAPQKDQDTGQTPGPN
                                                                                                                                                                                                                                                                                        ----ITPADAGVYYC------VKFRKEERGDMEFKSGPGTHLTVSAKPSPPV
                                                                                                                                                                                                                                                                                                                                                           ----PGREFIYSQKEAPFPRVTNVSDATKKN------NMDFSIRISN------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSSKSWITFDLKNKEVSVKRVTODPKLOMGKKLPLHLTLPQALP-----QYAGSGNLTLA
                                 LYSKLTYDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGEL----
                                                                   VPPTL-BITGSPSAGNQVNVTCQVNKFYPRHLQLTWLENGNMSRTEAASVFVENKDGTFN
                                                                                                                                                                                                                                                   LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH--EDPEVKFNWYVDGVEVHNAKTKPR
                                                                                                                                                                                                                                                                                                                        EKPVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVEPKSCDKTH-TCPPCPAPEL
                                                                                                        LPPSRDELT-----KNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF
                                                                                                                                            PEDNNVSYSINSTTKVLLATGDVHSQVICEVAHVTLQGGPPL-----RGTANLSETIR
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Pred. No. 8.3e<sup>.</sup>
70; Mismatches
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Pfam; PF00047; ig; 5.

PRINTS; PR01474; ICAMVCAM1.

PRINTS; PR01474; VCAM1.

SMART; SM00408; IGC2; 3.

PROSITE; P850835; IG_LIKE; 5.

Immunoglobulin domain; Glyco
Repeat; Signal.

SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Vascular cell adhesion protein 1 precursor (V-CAM
VCAM1 OR VCAM-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M84488; AAA42332.1; -. PIR; JS0675; JS0675. HSSP; P19320; IVCA.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Burkly L., Miyake K., Kincade P., Lobb
                                                                                                                                                                                                                                                                                                                                              InterPro; IPR007110; Ig-1Tke.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003989; VCAM-1.
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SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.
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CYTOPLASMIC (POTENTIAL).
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Best Local S
Matches 124
                                                                                                                                                                                             FGEM HUMAN STANDARD; PRT; 4391 AA. P98150; Q16287; Q9H3V5; Q1-0CT-1996 (Rel. 34, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Basement membrane-specific heparan sulfate protein precursor (HSPG) (Perlecan) (PLC).
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MEDLINE=92112994;
                                                                                                            Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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Pred. No. 0.00
37; Mismatches
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                                                                                                            Craniata; V
Catarrhini;
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                                                                                                                                  Vertebrata;
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                                                                                                              Hominidae;
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SEQUENCE OF 1-21 KKUP, A....
MEDLINE=94052171; PubMed=8234307;
Cohen I.R., Graessel S., Murdoch A.D., Iozzo
Cohen I.R., Graessel S., Murdoch A.D., Iozzo
                                                                                                                             Zhang H., Li X.-J., Martin D.B., Aebersold R.;
"Identification and quantification of N-linked glycoproteins using hydrazide chemistry, stable isotope labeling and mass spectrometry.";
Nat. Biotechnol. 21:660-666(2003).
-!- FUNCTION: This protein is an integral component of basement membranes. It is responsible for the fixed negative electrostatic charge and is involved in the charge-selective ultrafiltration properties. It serves as an attachment substrate for cells.
-!- SUBUNIT: Purified perlecan has a strong tendency to aggregate in dimers or stellate structures. It interacts with other basement
                                                                                                                                                                                                                                                                                                  CARBOHYDRATE-LINKAGE SITE ASN-2121.
MEDLINE-22660472; PubMed=12754519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning of human heparan sulfate proteoglycan core assignment of the gene (HSPG2) to 1p36.1-->p35 and a BamHI restriction fragment length polymorphism.", Genomics 11:389-396(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Fibrosarcoma;
MEDLINE=92120660; PubMed=1685141;
Kallunki P., Eddy R.L., Byers M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cloning, cellular expression, and mapping short arm of human chromosome 1."; Genomics 10:673-680(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 22-4391 FROM N.A., AND VARIANT SJS1 TYR-19 MEDLINB=20553141; PubMed=11101850; Nicole S., Davoine C.-S., Topaloglu H., Cattolico L., Beighton P., Ben-Hamida C., Hammouda H., Cruaud C., Wisamson D., Urtizberea J.A., Lehmann-Horn F., Weissenbarbentati F., Fontaine B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-92235084; PubMed=1569102; Murdoch A.D., Dodge G.R., Cohen I., Tuan R.S., Iozzo R.V.; Murdoch A.D., Dodge G.R., Cohen I., Tuan R.S., Iozzo R.V.; Primary structure of the human heparan sulfate proteoglycan from basement membrane (HSPG2/perlecan). A chimeric molecule with multiplomains homologous to the low density lipoprotein receptor, laminin, neural cell adhesion molecules, and epidermal growth factor."; J. Biol. Chem. 267:8544-8557(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Human basement membrane heparan sulfate proteoglycan core protein: 467-kD protein containing multiple domains resembling elements of the low density lipoprotein receptor, laminin, neural cell adhesion molecules, and epidermal growth factor.";

J. Cell Biol. 116:559-571(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUBECOTOM,
MEDLINE=91365376; PubMed=1679749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Perlecan, the major proteoglycan of basement membranes, patients with Schwartz-Jampel syndrome (chondrodystrophint. Genet. 26:480-483(2000).
                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                      its promoter.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ryggvason
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Heparan sulfate proteoglycan of human
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SUBCELLULAR LOCATION: Extracellular. TISSUB SPECIFICITY: Found in the bas PTM: CONTAINS THREE HEPARAN SULFATE AND O-LINKED OLICOSACCHARIDES.
DISEASE: Defects in HSPC2 are the ca syndrome (SUS1) [MIM:255800]; a rare
                                                                                                     membrane
IV.
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Iozzo R.V.;
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PÉAM; PF00057; Idl TECEPTCA; 4.

PÉAM; PF01390; SEA; 1.

PERINTS; PR00266; LDLRECEPTOR.

PRONTS; PR00231; Laminin_B; 3.

SMART; SM00181; EGF; 15.

SMART; SM00180; EGF; Lam; 12.

SMART; SM00408; IGC2; 21.

SMART; SM00408; IGC2; 21.

SMART; SM00281; LamB; 3.

SMART; SM00200; EGF; 1.

SMART; SM00200; EGF; 1.

PROSITE; PS001022; EGF 1; 9.

PROSITE; PS001025; LAM G DOMAIN; 3.

PROSITE; PS0025; LAM ININ TYPE_EGF; 11

PROSITE; PS00264; LDRAA 2; 4.

PROSITE; PS00264; SEA; 1.

PROSITE; PS00264; SEA; 1.
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EMBL; M64283; AAA52899.1; -.
EMBL; CAC436; AAB21121.2; -.
EMBL; L22078; -; NOT_ANNOTATED_CDS.
PIR; A38096; A38096.
HSSP; P00740; IEDM.
Siena-2DPAGE; P98160; -.
Genew; HGNC:5273; HSPG2.
MIM; 142461; -.
MIM; 255800; -.
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Pfam;
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- SIMILARITY: Contains 4 LDL-receptor class A domains.

- SIMILARITY: Contains 11 laminin EGF-like domains.

- SIMILARITY: Contains 3 laminin IV domains.

- SIMILARITY: Contains 22 immunoglobulin-like C2-type domains.

- SIMILARITY: Contains 3 laminin G-like domains.

- SIMILARITY: Contains 4 EGF-like domains.

- SIMILARITY: Contains 1 SEA domains.
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PF00053;
PF00054;
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; ig; 22.
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; laminin_G; 3.
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EVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLN----PEAGMWQCLLSDSGQVLLESNI
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                                                              EYVCRVMGSSGPLEASV-LVTIEASGSSAVHVPAPGGAPPIRIEPSSSRVAEGQTLDLKC
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LDL-RECEPTOR CLASS I
LDL-RECEPTOR CLASS I
LDM-RECEPTOR 1.
IG-LIKE C2-TYPE 1.
LAMININ EGF-LIKE 1
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POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                       RGKNIQG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IN EGF-LIKE 2.
IN EGF-LIKE 3 (INCOMPLETE)
IN EGF-LIKE 4 (INCOMPLETE)
IN EGF-LIKE 5 (N-TERMINAL).
IN DOMAIN IV 2 (DOMAIN III B
IN EGF-LIKE 5 (C-TERMINAL).
IN EGF-LIKE 7.
IN EGF-LIKE 7.
IN EGF-LIKE 9 (N-TERMINAL).
IN EGF-LIKE 9 (C-TERMINAL).
IN EGF-LIKE 10.
IN EGF-LIKE 10.
IN EGF-LIKE 11.
IN EGF-LIKE 12.
IN EGF-LIKE 11.
IN EGF-LIKE 11
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1 (DOMAIN III .
1 (C-TERMINAL).
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RESULT 62
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                              use
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                                                           between
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
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MEDLINE=83014953; PubMed=6812053;

Selsing E., Miller J., Wilson R., Storb U.;

Selsing E., miller J., Wilson R., Storb U.;

"Evolution of mouse immunoglobulin lambda genes.";

"Evolution of mouse immunoglobulin lambda genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Ig lambda_1 chain C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P01843;
21-JUL-1986
                modified
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                                                                                                                                                                                                                      MEDLINE=71107854;
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                                                                                                                                                                                                                                                                                                                          MEDLINE=82220143;
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=81148806;
                                                                                                                                                                                        "Amino
                                                                                                                                                                                                                                                                  Nature
                                                                                               ino acid sequences of two mouse immunoglobulin lambda chains."; C. Natl. Acad. Sci. U.S.A. 68:590-594(1971).

MISCELLANEOUS: The MOPC 315 cell line produces 2 light chains, normal lambda-2 chain and 1 abnormal lambda-1 chain that is missing a large part of the V region. The C region sequence (sl here) appears completely normal.

SIMILARITY: Contains 1 immunoglobulin-like domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      musculus (Mouse)
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PubMed=5276767;
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http://www
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Best Local
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001761; Q17362;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation updat
Waterston R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: Structural component of the muscle M-line. Myofilament lattice assembly begins with positional cues laid down in the hassement membrane and muscle cell membrane. UNC-89 responds to
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DISULFID
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SMART; SM00407; IGc1; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                            STRAIN-Bristol N2;
Du Z., Le T.T., Wilson
Submitted (MAY-1997) to
                                                                                                                                                                                                                                                          Muscle M-line ass
UNC-89 OR C09D1.1
                                                                                                                                                                                                                                                                                                                              CAEEL
                                                                                                                                      assembly, encodes a giant transduction domains.";
                                                                                                                                                        Benian G.M., Tinley T.L., Tang X., Borodovsky M., "The Caenorhabditis elegans gene unc-89, required
                                                                                                                                                                                                                 NCBI_TaxID=6239
                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                 Caenorhabditis elegans.
                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                              MEDLINE=96180278;
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                                                          REVISIONS
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InterPro; IPR003006;
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AAB59672.1;
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Ig_MHC.
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                                                                             EMBL/GenBank/DDBJ
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S -> SS (IN REF. 4)
E -> Q (IN REF. 4)
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Q -> E (IN REF. 4).
MISSING (IN REF. 4)
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3D-structure.
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Wormbep; COSD1.1; CE30426.

InterPro; IPR008957; FN III-like.

InterPro; IPR003961; FN III.

InterPro; IPR003961; FN III.

InterPro; IPR003109; Ig-like.

InterPro; IPR003109; Ig-MIC.

InterPro; IPR003006; Ig-MIC.

InterPro; IPR001849; PH.

InterPro; IPR007850; RCSD.

InterPro; IPR007850; RCSD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00041; fn3; 1.
Pfam; PF00047; 1g; 47.
Pfam; PF000169; PH; 1.
Pfam; PF00177; RCSD; 5.
Pfam; PF00177; RCSD; 5.
Pfam; PF000621; RhoGEF; 1.
Pfam; PF00018; SH3; 1.
SMART; SM00408; IGC2; 23.
SMART; SM00325; RhoGEF; 1.
SMART; SM00326; SH3; 1.
PROSITE; PS50010; DH; 1.
PROSITE; PS50010; DH; 1.
PROSITE; PS50003; PH DOMAIN
PROSITE; PS50003; PH DOMAIN
PROSITE; PS50003; PH DOMAIN
PROSITE; PS50003; PH DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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M-line.
TISSUE SPECIFICITY: Localizes to the middle of A-bands.
SIMILARITY: Contains 1 DBL-homology (DH) domain.
SIMILARITY: Contains 1 fibronectin type III domain.
SIMILARITY: Contains 49 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 1 PH domain.
SIMILARITY: Contains 1 PH domains.
SIMILARITY: Contains 1 SH3 domains.
SIMILARITY: Contains 1 SH3 domains.
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; SH3; 1.
10; DH_2; 1.
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RCSD 5.
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10-OCT-2003 (Rel. 42, Last annotation
Ig lambda-2 chain C region.
Rattus norvegicus (Rat).
                                                                                           Interpro; IPR007110; Ig-like.
Interpro; IPR003597; Ig_c1.
Interpro; IPR003006; Ig_MHC.
                                                                                                                                                                                    EMBL; M22521; AAA41420.1; ALT_INIT HSSP; P01842; 2MCG.
                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/ar
                                                                                                                                                                                                                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                                                                                                                                                                                This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Steen M.L., Hellman L., Pettersson U.;
"The immunoglobulin lambda locus in ra
genes and a single V lambda gene.";
Gene 55:75-84(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=87305594; PubMed=3114047;
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RESULT
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Best Local S
Matches 36
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MOUSE
PGBM MOUSE
Q05793;
                                                                                                                                                                                               Noonan D.M., Horigan E.A., Ledbetter S.R., Vogeli G., Sasaki M., Yamada Y., Hassell J.R.;

Yamada Y., Hassell J.R.;

"Identification of cDNA clones encoding different domains of the basement membrane heparan sulfate proteoglycan.";

J. Biol. Chem. 263:16379-16387(1988).

-I-FUNCTION: This protein is an integral component of basement membranes. It is responsible for the fixed negative electrostatic charge and is involved in the charge-selective ultrafiltration properties. It serves as an attachment substrate for cells.

-I-SUBUNIT: Purified perlecan has a strong tendency to aggregate in dimers or stellate structures. It interacts with other basement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoglobulin on NON TER 1
DOMAIN 6
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DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Basement membrane-specific heparan sulfate proteoglycan
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 940-1601 AND 1870-2600 FROM N.A., MEDLINE=89034110; PubMed=2972708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  sulfate proteoglycan, reveals extensive similarity with laminin A chain, low density lipoprotein-receptor, and the neural cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Noonan D.M., Fulle A., Valente P., Yamada Y., Hassell J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein precursor (HSPG)
-!- SUBCELLULAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: Found in the basement mem
-!- PTM: COUVAINS THREE HEPARAN SULFATE CHAINS AS
AND O-LINKED OLIGOSACCHARIDES.
-!- SIMILARITY: Contains 4 LDL-receptor class A de
-!- SIMILARITY: Contains 11 laminin EGF-like doma
-!- SIMILARITY: Contains 3 laminin IV domains.
-!- SIMILARITY: Contains 15 immunoglobulin-like Co-
-!- SIMILARITY: Contains 15 immunoglobulin-like Co-
-!- SIMILARITY: Contains 1 EGF-like domain.
-!- SIMILARITY: Contains 1 SEGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92078153; PubMed=1744087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'The complete sequence of perlecan, a basement membrane
                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. Chem. 266:22939-22947(1991).
                                                                                                                                                                                       membrane components such as laminin,
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 Contains 4 LDL-receptor class A domains. Contains 11 laminin EGF-like domains. Contains 3 laminin IV domains.
Contains 15 immunoglobulin-like C2-type Contains 3 laminin G-like domains.
Contains 1 EGF-like domain.
Contains 1 EGF-like domain.
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Rodentia;
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Pred. No. 0
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DR InterPro; IPR000985; ConA like_lec_gl.

InterPro; IPR000742; EGF 7.

DR InterPro; IPR000742; EGF 7.

DR InterPro; IPR000710; Ig-Tike.

DR InterPro; IPR000710; Ig-Tike.

DR InterPro; IPR000710; Ig-Tike.

DR InterPro; IPR000034; Laminin_B.

InterPro; IPR000034; Laminin_B.

DR InterPro; IPR000719; Laminin_B.

InterPro; IPR000192; ESA_domain.

DR InterPro; IPR000192; ESA_domain.

DR Pfam; PF00052; Iaminin_G; 3.

DR Pfam; PF00053; laminin_G; 3.

DR Pfam; PF00054; Laminin_G; 3.

DR Pfam; PF00057; Idl_recept_a; 4.

DR Pfam; PF00057; Idl_recept_a; 4.

DR Pfam; PF00051; Laminin_G; 3.

DR Pfam; PF00051; Laminin_G; 3.

DR Pfam; PF00051; Laminin_G; 3.

DR Pfam; PF00052; Laminin_G; 3.

DR Pfam; PF00053; Laminin_G; 3.

DR Pfam; PF00051; Laminin_G; 3.

DR Pfam; PF00052; Laminin_G; 3.

DR PROSITE; PS00126; EGF 1; 8.

DR PROSITE; PS00126; EGF 1; 8.

DR PROSITE; PS0025; LAM_G_DOMAIN; 3.

DR PROSITE; PS0025; LAM_G_DOMAIN; 3.

DR PROSITE; PS0026; LAMININ_TYPE_EGF; 11.

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REMBL; J04054; AAA3989.1; -.

REMBL; J04055; AAA39912.1; -.

REMBL; J04055; AAA3999.1; -.

REMBL; J04055; AAA39912.1; -.

REMBL; J04055; AAA3912.1; -.

REMBL; J04055; AAA39912.1; -.

REMBL; J04055; AAA3912.1; -.

REMBL; J04055; AAA3912.1; -.

REMBL; J04055; AAA3912.1; -.

REMBL; J04055; AAA39912.1; -.

REMBL; J04055; AAA39912.1
        DOMAIN
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04054; AAA39899.1; -.
04055; AAA39912.1; -.
        194
234
319
369
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813
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1126
LDL-RECEPTOR CLASS A 1.

LDL-RECEPTOR CLASS A 2.

LDL-RECEPTOR CLASS A 3.

LDL-RECEPTOR CLASS A 3.

LDL-RECEPTOR CLASS A 4.

LDL-RECEPTOR CLASS A 4.

IG-LIKE C2-TYPE 1.

LAMININ EGF-LIKE 1 (N-TERMINAL).

LAMININ EGF-LIKE 1 (C-TERMINAL).

LAMININ EGF-LIKE 2.

LAMININ EGF-LIKE 3.

LAMININ EGF-LIKE 4 (INCOMPLETE).

LAMININ EGF-LIKE 5 (N-TERMINAL).

LAMININ EGF-LIKE 5 (N-TERMINAL).

LAMININ EGF-LIKE 5 (C-TERMINAL).

LAMININ EGF-LIKE 5 (C-TERMINAL).

LAMININ EGF-LIKE 5 (C-TERMINAL).
                                                                                                                                                                                                                                                                                                        SULFATE
SEA.
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PROTEOGLYCAN CORE PROTEIN.
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KE 1 (N-TERMINAL).

N IV 1 (DOMAIN III ?

IKE 1 (C-TERMINAL).
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LAMININ EGF-LIKE 9 (N-TERMINA LAMININ EGF-LIKE 9 (C-TERMINA LAMININ EGF-LIKE 9 (C-TERMINA LAMININ EGF-LIKE 10.

LAMININ EGF-LIKE 11.

LAMININ EGF-LIKE 12.

LAMININ EGF-LIKE 12.

LAMININ EGF-LIKE 12.

LAMININ EGF-LIKE 13.

LAMININ EGF-LIKE 14.

LAMININ EGF-LIKE 12.

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LAMININ EGF-LIKE 14.

LAMININ EGF-LIKE 12.

LAMININ EGF-LIKE 13.

LAMININ EGF-LIKE 13.

LAMININ EGF-LIKE 14.

LEGF-LIKE C2-TYPE 11.

LEGF-LIKE C2-TYPE 11.

LEGF-LIKE C2-TYPE 13.

LAMININ EGF-LIKE 3.

LEGF-LIKE C2-TYPE 11.

LEGF-LIKE C2-TYPE 12.

LEGF-LIKE C2-TYPE 13.

LEGF-LIKE C2-TYPE 14.

LEGF-LIKE C2-TYPE 11.

LEGF-LIKE C2-TYPE 12.

LEGF-LIKE C2-TYPE 11.

LEGF-LIKE C2-TYPE 12.

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LEGF-LIKE C2-TYPE 14.

LEGF-LIKE C2-TYPE 11.

LEGF-LIKE C2-TYPE 11.

LEGF-LIKE C2-TYPE 12.

LEGF-LIKE C2-TYPE 11.

LEGF-LIKE C2-TYPE 12.

LEGF-LIKE C2-TYPE 13.

LEGF-LIKE C2-TYPE 12.

LEGF-LIKE C2-TYPE 13.

LEGF-LIKE C2-TYPE 14.

LEGF-LIKE C2-TYPE 12.

LEGF-LIKE C2-TY
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IN EGF-LIKE 8 (N-TERMINAL).

IN EGF-LIKE 9 (N-TERMINAL).

IN DOMAIN IV 3 (DOMAIN III C)

IN EGF-LIKE 9 (C-TERMINAL).

IN EGF-LIKE 10.

IN EGF-LIKE 11.

KE C2-TYPE 2.

KE C2-TYPE 3.

KE C2-TYPE 5.

KE C2-TYPE 5.

KE C2-TYPE 6.

KE C2-TYPE 7.

KE C2-TYPE 10.

KE C2-TYPE 10.

KE C2-TYPE 11.

KE C2-TYPE 11.

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KE C2-TYPE 13.

KE C2-TYPE 14.

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Matches
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Best Local
                                                                                                                                                                         MOUSE
NEO1 MOUSE
P97798;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
DISULFID
DISULFID
MEDLINE=97407661; PubMed=9264410; Keeling S.L., Gad J.M., Cooper H.M.; "Mouse neogenin, a DCC-like molecule,
                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                               Mus musculus
                                                                                                                                      Neogenin
                                                                                                                                                 16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
10-OCT-2003 (Rel. 42,
                                                 SEQUENCE FROM N.A.,
                                                                        NCBI_TaxID=10090;
                                     SSUE=Brain,
                                                                                                                                                                                                                                                               2416
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                                                                                                                                                                                                                                                              SNVYGMAQSVVNLSVHGPPTVSVLPEGPVHVKMGKDITLECISSGEPRSSPRWT
                                                                                                                                                                                                                                                                                      GNVFSC--SVMHEALHNHYTQKSLSLSP-----GLQLDETCAEAQDGELDGLWT
                                                                                                                                                                                                                                                                                                             FKCLIHEGAMP--IKVEWKIRDQELEDNVHISP-----NGSIITIVAPGPATMEPTACVA 2415
                                                                                                                                                                                                                                                                                                                                     LTCLV-KGFYPSDIAVEWESNGQP-ENNYKTTPPVLDSDGSFFLY---SKLTVDKSRWQQ
                                                                                                                                                                                                                                                                                                                                                                                     QDWLNGKEYKCKVSNKALP---APIEKTISKAKGQP---REPQVYTLPPSRDELTKNQVS
                                                                                                                                                                                                                                                                                                                                                                                                             LTEGQTVDLKCVVPGQAH----AQVTWHKRG----SSLPARHQTHGSLLRLYQLSPA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSK 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -LRLHHMSVADSGEYVCRANNNIDAQETSIMISVSPSTNSPPAPASPAPIRIESSSSRVA 2064
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                                                                                                               (Mouse)
                                                                                                                                                                                                                                                                                                                                                              -DSGEYVCQVAGSSHPEHEASFKLTVPSSQNSSFRLRSPVISIEPPSSTVQQGQDAS
                                                                                                                                                                                                   STANDARD;
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17.7%;
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Last
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                                                                                                                                                  annotation
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Pred. No. 0.01
94; Mismatches
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                                                                                    Craniata; Vertebrata; I
Sciurognathi; Muridae;
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                                                   SPLICING
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 has four splice variants and
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Pfam; PF00041; fn3; 6.—
Pfam; PF00047; ig; 4.
Pfam; PF00014; FNTYPEIII.
SMART; SM00060; FN3; 6.
SMART; SM00408; IGC2; 4.
PROSITE; PS50835; IG_LIKE; 4.
Ccll adhesion; Repeat; Signal; T)
                                                                                                                              DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expressed widely in the adult mouse and during embryogenesis.";
Oncogene 15:691-700(1997).

-i-FUNCTION: May be involved as a regulatory protein in the transition of undifferentiated proliferating cells to their differentiated state. May also function as a cell adhesion molecule in a broad spectrum of embryonic and adult tissues.

-i-SUBCELLULAR LOCATION: Type I membrane protein.
                DOMAIN
DOMAIN
                                            DOMAIN
DOMAIN
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DOMAIN
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DOMAIN
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HSSP; P02751; 1TTF.
MGD; MGI:1097159; Neo1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                       Glycoprotein;
                                                                                                                                                                                                                                                                                                                               InterPro; IPR008957; FN III-like.
InterPro; IPR003961; FN III.
InterPro; IPR003962; Fn III subd.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                     InterPro; IPR007110;
InterPro; IPR003598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND E16.5.
- SIMILARITY:
- SIMILARITY:
- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISOId=P97798-5; Sequence=VSP_002597;
Note=Expression developmentally regulated;
TISSUE SPECIFICITY: Widely expressed.
DEVELOPMENTAL STAGE: EXPRESSED UBIQUITOUSLY THROUGHOUT THE MID TO LATE STAGES OF GESTATION AND IN ADULT TISSUES. STRONG EXPRESSION IS OBSERVED IN THE VENTRAL REGION OF THE VENTRICULAR ZONE OF THE E15.5 MOUSE NEURAL TUBE, AS WELL AS IN THE VENTRICULAR ZONES OF THE MESSENCEPHALON AND RHOMBENCEPHALON. ISOFORMS 3 AND 4 ARE EXPRESSED AT HIGHER LEVEL COMPARED TO OTHER ISOFORMS BETWEEN E11.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Type I membrane protein ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note=Expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=P97798-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Comment=Additional isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=P97798-4;
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Contains 6 fibronectin type III domains.
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developmentally regulated;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the immunoglobulin superfamily.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
FIBRONECTIN TYPE-III 1
FIBRONECTIN TYPE-III 3
FIBRONECTIN TYPE-III 3
FIBRONECTIN TYPE-III 4
                                                                                                                                             EXTRACELLULAR POTENTIAL.
                                                                                                                                 CYTOPLASMIC
                                                                                                                                                                                                                   Transmembrane;
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                                                                             NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS-----
                                                                                                                     CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
                                                                                                                                        HNLQVLGLVKSDEGFYQCIAENDVGNAQAGAQLIILEHDV-AIPT-LPPTSLTSATTDHL
                                                                                                                                                                               LTVQVPPGFLKQPANIYAHESMDIV--FECEVTGKPTPTVKWVKNGDVVIPSDNFKIVKE
                                                                                                                                                                                                                                          SKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQY---AGSGNLT-----
                                                                                                                                                                                                                                                                                                      NADLVPFVRWEQNRQPLLLDDRIVKLPSG-TLVISNATEGDGGLYRCIVESGGPPKFSDE
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PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL---
                  IFKVMAQNKHGSGESSAPLRVE-TQPEVQLPGPAPNIRAYATSPTSITVTWETPLSGNGE
                                                                                                   APATTGP-
                                                                                                                                                            E--KPVWVLNPEAGMWQCLL-SDSGQ-----VLLESNIKVLPTWSTPVEPKSCDKTHT
                                                                                                                                                                                                    LALEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLML----SLKLENKEAKVSKR
                                                                                                                                                                                                                                                               AELKVLQDPEEIVDLVFLMRPSSMMKVTGQ----SAVLPCVVSGLPAPVVRW------
                                                                                                                                                                                                                                                                                   VEFKI-----DIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASS
                                                                                                                                                                                                                                                                                                                         PPGSSPSV---QCRSP----RGKNIQGGKTLSVSQLELQDSGTWTCTVLQN-----QKK
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                                      -- KAKGQPREPQVYTLPPSRDELTKNQVSL----TCLVKGFYPSDIAVEWES----NGQ
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Pred. No. 0.0088;
9; Mismatches 282;
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441DE919D5E17C0E CRC64;
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AC PO1845;
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DT 21.JUL-1986 (Rel. 01,
DT 21.JUL-1986 (Rel. 01,
DT 10-OCT-2003 (Rel. 42,
DE 19 lambda-3 chain C re
OS Mus muscullus (Mouse).
CE LINEARYOTA; Metazoa; CP
OC MAMMALIA; Butheria; RC
OX NCBI_TAXID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83014953; Pubh
RA Selsing E., Miller J.,
RY "Evolution of mouse in
RL Proc. Natl. Acad. Sci.
RN [2]
RP SEQUENCE OF 1-18 (MYEE
RA SEQUENCE OF 1-18 (MYEE
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Matches 35
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SMART; SM00407; IGcl; 1.
PROSITE; PS0035; IG LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=83014953; PubMed=6812053;
Selsing E., Miller J., Wilson R., Storb U.;
"Evolution of mouse immunoglobulin lambda genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:4681-4685(1982).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; J00585; AAB59670.1; -.
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Azuma T., Steiner L.A., Eisen H.N.;
RIdentification of a third type of lambda light
immunoglobulins.";
Proc. Natl. Acad. Sci. U.S.A. 78:569-573(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-18 (MYSLOMA PROTEIN CBPC-49).
Breyer R.M., Sauer R.T., Elsen H.N.;
Breyer R.M., Sauer R.T., Elsen H.N.;
"The variable region of mouse lambda-3 chains.";
ICN UCLA Symp. Mol. Cell. Biol. 20:105-110(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains 1 immunoglobulin-like domain.
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QPRE-PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
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IPR003597; Ig_c1.
IPR003006; Ig_MHC.
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34.3%;
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                                                                       Score 163; DB 1;
Pred. No. 0.00038;
6; Mismatches 47
                                                                                                                                                                                                           INTERCHAIN (WITH HEAVY CHAIN)
                                                                                                                                                                                                                                                             IG-LIKE.
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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Bistchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1990
01-APR-1990
15-MAR-2004
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                                                                 MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genomic structure of the human Ig lambda 1 gene suggests that it me be expressed as an Ig lambda 14.1-like protein or as a canonical B cell Ig lambda light chain: implications for Ig lambda gene
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MEDLINE=91108327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expressed in pre-B cells and omega light-chain protein."; Proc. Natl. Acad. Sci. U.S.A.
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MEDLINE=89315835; PubMed=2501791;
Hollis G.F., Evans R.J., Stafford-Hollis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAR-2004 (Rel. 43, Last annotation update)
Immunoglobulin lambda-like polypeptide 1 precursor (Immunoglobulin-related 14.1 protein) (Immunoglobulin omega polypeptide) (Lambda 5)
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P15814;
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                                               WWW="http://www.ncbi.nlm.nih.gov/prow/guide/696419174_g.htm"
SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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Sci. U.S.A.
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e human immunoglobulin
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RESULT 69
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Best Local
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P20273; O95699; O95701; O95702; O95703; Q01665;
O9UQA7; O9UQA8; O9UQA9; O9UQA9; O9YZA6;
O1-FEB-191 (Rel. 17, Created)
15-JUL-199 (Rel. 38, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
B-cell receptor CD22 precursor (Leu-14) (B-lymph
molecule) (BL-CAM) (Siglec-2).
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EMBL; M34513; AAA36096.1; -.
EMBL; M34511; AAA36096.1; JOINED.
EMBL; M34512; AAA36096.1; JOINED.
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                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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EMBL; BC012293; AAH12293.1;
PIR; A33911; A33911.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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GO; GO:0006955;
         SEQUENCE FROM N.A.
                                            cell interactions
                                                     Wilson G.L., Fox C.H 
"CDNA cloning of the
                                                                           MEDLINE=91086838; PubMed=1985119;
                                                                                        TISSUE=Tonsil
                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
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                                                                                                  SEQUENCE FROM N.A.
                                                                                                                      NCBI_TaxID=9606;
                               Exp. Med. 173:137-146(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                            Signal;
                                                                                                                                                                                                                                                                                                                                       SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQ 636
                                                                                                                                                                                                                                                                                                                  SNNKYAASSYLSITPEOWRSRRSYSCOVWHE-----GSTVEKTVAPAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 AA;
                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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97
                                                                                                                                                       (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C:membrane; NAS.
F:defense/immunity
P:immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin domain.
                                                     he B
                                                                                                                                                                          74, Last annotation update)
22 precursor (Leu-14) (B-lymphocyte cell adhesion (Siglec-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213
108
          (ISOFORMS CD22-ALPHA
                                                                                                  (ISOFORM CD22-BETA),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213
                                                                                                                                  Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    22963
                                                                                                                                                                                                                                                                                                                                                                                                                   4.8%;
                                                     Fauci A.S., K cell membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WW;
                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                                        Score 162.5;
Pred. No. 0.00
21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIGHT CHAIN).

C REGION (BY SIMILARITY TO LIGHT-CHAIN).

; 9133A7742B943C79 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIGHT-CHAIN)
C REGION (RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.

IMMUNOGLOBULIN LAMBDA-LIKE
J REGION (BY SIMILARITY TO
                                                                                                                                  Craniata; Vertebrata; Catarrhini; Hominidae;
                                                    Kehrl J.H.
ne protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein activity;
           AND
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           CD22-BETA)
                                                                                                   VARIANT HIS-639
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                                                                                                                                                                                                                                                Q92872; Q92873;
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                      mediator
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                                                      of B-B
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MEDLINE=93267103; PubMed=8496602;

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A Tredder T.F., Tuscano J., Sato S., Kehrl J.H.;

A Tredder T.F., Tuscano J., Sato S.,

T "CD22, a B lymphocyte-specific adhesion molecule that regulates

T antigen receptor signaling.";

I Annu. Rev. Immunol. 15.481-504 (1997).

C -!- FUNCTION: Mediates B-cell B-cell interactions. May be involved in the localization of B-cells in lymphoid tissues. Binds sialylated C glycoproteins; one of which is CD45. Preferentially binds to C alpha2,6-linked sialic acid. The sialic acid recognition site can be masked by cis interactions with sialic acids on the same cell surface. Upon ligand induced tyrosine phosphorylation in the imune response seems to be involved in regulation of B cell antigen receptor signaling. Plays a role in positive regulation through interaction with Src family tyrosine kinases and may also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STALIC ACID BINDING.

MEDLINE=93216636; PubMed=8463235;

MEDLINE=93216636; PubMed=8463235;

MEDLINE=93216636; PubMed=8463235;

MEDLINE=93216636; PubMed=8463235;

MEDLINE=93216636; PubMed=8463235;

MEDLINE=93216636; PubMed=8463235;

MEDLINE=93216636; Varki A.;

MEDLINE=93216636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Law C.L., Sidorenko S.P., Chandran K.A., Zhao Z., SFischer E.H., Clark E.A., "Clark E.A.," Clark E.A., "Clark E.A.," Protein tyrosine phosphatase phospholipase C-gamma(1) upon B cell activation.", J. Exp. Med. 183:547-560(1996).
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INTERACTION WITH PTPN6.
MEDLINE=95343349; PubMed=7618087;
MEDLINE=95343349; PubMed=7618087;
Instance of the control of the
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[5]
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Garcia E., Kyle A., Ramirez M., Stilwagen S., Garnes J.,
Danganan L., Bruce R., Quan G., Montgomery M., Ow D.,
Kobayashi A., Olsen A.O., Carrano A.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tuscano J.M., Engel P., Tedder T.F., Agarwal A., "Involvement of p72syk kinase, p53/56lyn kinase inositol-3 kinase in signal transduction via the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thomas M.L., Fearon D.T.;
"A role in B call activation phosphatase SHP.";
Science 269:242-244 (1995).
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VARIANTS THR-34; GLU-152; LYS-203; GLY-664; CYS-669
MEDLINE=99180618; PubMed=10079291;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERACTION WITH PTPN6; SYK AND PLCG1.
MEDLINE=96195207; PubMed=8627166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERACTION WITH LYN; SYK AND PIP
MEDLINE-96257803; PubMed-8647200;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97288746; PubMed=9143697;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chandran K.A., Zhao Z.,
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kinase and phosphatidyl
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modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch). the European Bioinformatics Institute. Th act as an inhibitory receptor by recruiting cytoplasmic phosphatases via their SH2 domains that block signal transduthrough dephosphorylation of signaling molecules.

1. SUBUNIT: Predominantly monomer of isoform CD22-beta. Also for the terodimer of isoform CD22-beta and a shorter isoform. Interacts with GRB2, INPPSD and SHC1 upon phosphorylation. Interacts with GRB2, INPPSD and SHC1 upon phosphorylation (By similarity). May form a complex with INPPSD/SHIP, GRB2 and SHC1.

1. SUBCRLUILAR LOCATION: Type I membrane protein.

1. ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2; PTM: Phosphorylated on tyrosine residues by LYN (By SIMILARITY: Belongs to the immunoglobulin superfami (sialic acid binding Ig-like lectin) family.

SIMILARITY: Contains 6 immunoglobulin-like C2-type SIMILARITY: Contains 1 immunoglobulin-like V-type d CAUTION: Ref.4 sequence differs from that shown due frameshift in position 806. Name=CD22-alpha;
IsoId=P20273-2; Sequence=VSP_002531;
ISOId=P20273-2; Sequence=VSP_002531;
TISSUE SPECIFICITY: B lymphocytes.
DOMAIN: Contains 4 copies of a cytoplasmic motif that is referred to as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in downmodulation of cellular responses. The phosphorylated ITIM motif binds to the SH2 domain of PTPN6/SHP-1. DATABASE: NAME=PROW; NOTE=CD guide CD22 entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd22.htm". PTM: Phosphorylated both on threonine/serine and tyrosine Name=CD22-beta; residues SWISS-PROT entry is copyright. It is produced through a collaboratic sen the Swiss Institute of Bioinformatics and the EMBL outstation Comment=Additional isoforms IsoId=P20273-1; Sequence=Displayed seem There are no restrictions ong as its content is in to exist; . Usage by and for http://www.isb-sib superfamily. LYN (By signal transduction due SHC1 upon domain. ue to a domains. similarity). Also SIGLEC for Interacts collaboration L outstation -5 9

EMBL; X59350; CAA42006.1; -. ch/announce,

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EMBL; U62631; AAB06448.1; --
EMBL; U62631; AAB06449.1; --
EMBL; K52785; CAA36988.1; ALT_FRAME.
EMBL; AB012996; BAA36565.1; --
EMBL; AB012997; BAA36566.1; --
EMBL; AB012999; BAA36568.1; --
EMBL; AB012999; BAA36568.1; --
EMBL; AB012999; BAA36568.1; --
EMBL; AB012999; BAA36571.1; --
EMBL; AB013000; BAA36577.1; --
EMBL; AB013004; BAA36577.1; --
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PROSITE; PS50835; IG_LIKE; 6.
Cell adhesion; Lectin; Antigen;
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                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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-ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG
                            SNPSVTRYEW-----KPHGAWEEPS-----LGVLKIQNVGWDN-TTIACAACNSW
                                             EDPEV-KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK-
                                                                                                      VQYAPEPSTVQILHSPAVEGSQVEFLCMSLANPLPTNYTWYHNGKEMQGRTEEKVHIPKI
                                                                                                                                           PEYTTVSWLKDGTSLKKQN-TFTLNLRE----VTKDQSGKYCCQVSNDVGPGRSEEVFLQ
                                                                                                                                                           PKLM-----LSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSD-----
                                                                                                                                                                                HGKIVTCQLQDADGKFLSNDTVQLNVKHTPKLEIKVTPSDAIVREGDSVTMTCEV-SSSN
                                                                                                                                                                                                   SGNL-TLALEAKTGKL--HQEVNLVVMRATQLQ------KNLTCEVWGPTS
                                                                                                                                                                                                                      ---QLQWLLEGVPMRQAAVT----STSLTIKSVFTRSELKFS--
                                                                                                                                                                                                                                        GSGELWWQAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAG
                                                                                                                                                                                                                                                         KTEKWMERIHLNVSERPFPPHIQLPPEI---QESQEVTLTCLLNFSCYGYPI-----
                                                                                                                                                                                                                                                                            KVEFKIDIVVL-----AFQKASSIVYKKEGEQVE-----FSFPLAFTVEKLT
                                                                                                                                                                                                                                                                                                FDGTRLYESTKDGKVPSEQKRVQFLGDKNKNC----TLSIHPVHLNDSGQ---LGLRMES
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                                                                 LPWHAGTYSCVAENILGTGQRGPGAELDVQYPPKKVTTVIQNPMPIREGDTVTLSCNYNS
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PIK3R1/PIK3R2) (BY SIN
N-LINKED (GLCNAC. . .)
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IG-LIKE C2-TYPE 4
IG-LIKE C2-TYPE 5
IG-LIKE C2-TYPE 6
IG-LIKE C2-TYPE 6
ITH MOTIF 1.
ITIM MOTIF 3.
ITIM MOTIF 3.
ITIM MOTIF 4.
BY SIMILARITY.
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Pred. No. 0.0
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PHOSPHORYLATION
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RESULT
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Stapleton M., Some
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10-OCT-2003
Vascular cel
  TISSUE=Retinal pigment epithelium;

MEDLINE=22386257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE=91152090; PubMed=1715583;

MEDLINE=91152090; PubMed=1715583;

Cybulsky M.I., Fries J.W.U., Williams A.J., Sultan Cybulsky M.I., Fries J.W.U., Williams A.J., Sultan Byers M., Shows T., Gimbrone M.A. Jr., Collins T.;

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Proc. Natl. Acad. Sci. U.S.A. 88:7859-7863(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
                                                                                                                                            Rieder M.J., Armel T.Z.,
Rajkumar N.R., Toth E.J.
Submitted (AUG-2002) to
                                                                                                                                                                                                                                  "Cloning (VCAM1)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90090619; PubMed=2688898; Hession C., Tizard R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VCA1_HUI
P19320;
                                                                                                                                                                                                                                           MEDLINE=91201302; PubMed=1707873;
Hession C., Tizard R., Vassallo C.,
Chi-Rosso G., Luhowskyj S., Lobb R.,
"Cloning of an alternate form of vas
                                                                                                                                                                                                                                                                                                                                                                                                                                    Osborn L., Hession C., Tizard R., Vassallo Chi-Rosso G., Lobb R.; "Direct expression cloning of vascular cel cytokine-induced endothelial protein that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-91016951; PubMed=1699207;
Polte T., Newman W., Gopal T.V.;
"Full length vascular cell adhesion molecule
Nucleic Acids Res. 18:5901-5901(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VCAM1 OR L1CAM.
                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                            Cell 59:1203-1211(1989).
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(Rel. 16, Last sequence update,
(Rel. 42, Last annotation update)
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Primates;
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E.J., Yi Q., Nickerson
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Catarrhini; Hominidae;
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ckerson D.A.
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Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci u e n
         EMBL; X53051;
EMBL; M30257;
                                                                                       between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                     This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acta Crystallogr. D 52:369-379(1996).
-I- FUNCTION: IMPORTANT IN CELL-CELL RECOGNITION. APPEARS TO FUNCTION IN LEUKOCYTE-ENDOTHELIAL CELL ADHESION. INTERACTS WITH THE BETA-1 INTEGRIN VLA4 ON LEUKOCYTES, AND MEDIATES BOTH ADHESION AND SIGNAL TRANSDUCTION. THE VCAMI/VLA4 INTERACTION MAY PLAY A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang J.-H.,
Osborn L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The crystal structure of an N-terminal two-domain fragment vascular cell adhesion molecule 1 (VCAM-1): a cyclic peptid the domain 1 C-D loop can inhibit VCAM-1-alpha 4 integrin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jonne E.Y., Harlos K., Bottomley M.J., Robinson R.(
Edwards R.M., Clements J.M., Dudgeon T.J., Stuart I
"Crystal structure of an integrin-binding fragment
adhesion molecule-1 at 1.8-A resolution.";
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MEDLINE=95147978; PubMed=7531291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structure of a resolution.";
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                                                                                                                                                                                                                                                                                                         PTM: Sialoglycoprotein.

DISBASE: May play an important role in the genesis of artherosclerosis and rheumatoid arthritis.

artherosclerosis and rheumatoid arthritis.

SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.

DATABASE: NAME=PROW; NOTE=CD guide CD106 entry;

DATABASE: NAME=PROW; NOTE=CD guide CD106 entry;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           well as on macrophage-like and dendritic cell tand inflamed tissue.
INDUCTION: By cytokines (e.g. IL-1, TNF-alpha).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Type I membrane protein ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PATHOPHYSIOLOGIC ROLE BOTH IN IMMUNE RESPONSES EMIGRATION TO SITES OF INFLAMMATION.
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                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Natl. Acad. Sci. U.S.A.
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CAA37218.1; -.
AAA51917.1; ALT_TERM
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T., Pepinsky R.B., Liu J.-H.,
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J., Stuart D.I
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                                                                                                                                                                                                                                                           Repeat; Signal; SIGNAL 1
                                                                                                                                                                                                                                                                                 PRINTS; PR01472; ICAMVCAM1 PRINTS; PR01474; VCAM1. SMART; SM00408; IGC2; 3.
                                                                                                                                                                                                                                                                                                  InterPro; IPR003987; ICAM VCAM-1.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003999; VCAM-1.
Pfam; PF00047; ig; 6.
                                                                                                                                                                                                                                                                                                                                          PDB; 1VCA; 15-SEP-95.
PDB; 1VSC; 20-JUN-96.
PDB; 1IJ9; 07-NOV-01.
                                                                                                                                                                                                                                                                                                                                                                       EMBL; M73255; AAA61270.1; --
EMBL; M60335; AAA61269.1; --
EMBL; AF536818; AAM96190.1; --
EMBL; BC017276; AAH17276.1; --
                                                                                                                                                                                                                                                                                                                                MIM; 192225;
                                                                                                                                   VARSPLIC
                                                                                                                                                                                                                                                                            PROSITE; PS50835; IG_LIKE; 5.
                                                                                                                                                                                                                                                                                                                                       Genew;
                                                                                                                                                                                                                                                                      Immunoglobulin domain; Glycoprotein; Cell adhesion;
                                                                                                                                                                                                                                                                                                                                                            A41288; A41288.
B41288; B41288.
                                                                                                                                                                                                                                                                                                                                     HGNC:12663; VCAM1.
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                                                                                                                                        Alternative
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                                                                                                                                                                                                                                                                 splicing;
                                                                                                                                                                                           IG-LIKE C2-TYPE
                                                                                                                                       N-LINKED
N-LINKED
N-LINKED
                                                                                                                           Missing (in isoform /FTId=VSP_002580.
                                                                                                                                                                                                                                   POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                     N-LINKED
                                                                                                                                                                                                                                                VASCULAR CELL EXTRACELLULAR
                                                                                        FTId=VAR_014311
                                                                                                     FTId=VAR_014310
                                                                                                                FTId=VAR_014309
                                                                               FTId=VAR_014312
                                                                                                                                             (GLCNAC.
(GLCNAC.
(GLCNAC.
(GLCNAC.
                                                                                                                                                                                                                                                                Polymorphism;
                                                                                                                                         (GLCNAC.
                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                                                                                     ADHESION PROTEIN 1.
                                                                                                                                                                                             7654881
                                                                                                                                   Short).
                                                                                                                                                   (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                Transmembrane; 3D-structure.
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LAC2_N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IAC2_MOUSE STANDARD; PRT; 1

P01844;

21-JUL-1986 (Rel. 01, Created)

21-JUL-1986 (Rel. 01, Last sequence up

10-OCT-2003 (Rel. 42, Last annotation

Ig lambda-2 chain C region.
  Nature 298:380-382(1982)
                                                                                                                                                                                                                           Wu G.E., Govindji N., Hozumi N., Muri
"Nucleotide sequence of a chromosomal
immunoglobulin gene of mouse.";
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-83014953; PubMed=6812053;
Selsing E., Miller J., Wilson R., Storb U.;
"Evolution of mouse immunoglobulin lambda genes.
Proc. Natl. Acad. Sci. U.S.A. 79:4681-4685(1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                            Baltimore
                                                                                                 Bothwell A.L.M.,
                                                                                                                         MEDLINE=82220143;
                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                        Nucleic
                                                                                                                                                                                                                                                                                                       MEDLINE=82274221;
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                               "Somatic variants of murine immunoglobulin lambda light chains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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                                                                                               Paskind M., Reth
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PubMed=6283385;
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01-APR-1990
01-APR-1990
15-JUL-1999
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Dugan E.S., Bradshaw R.A., Simms E.S., E
"Amino acid sequence of the light chain of the light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HB2D
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SMART; SM00407; IGc1; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as zong ... Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this alicense agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Etropean Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content
                                                                                    MEDLINE=90361905; PubMed=2391424;
Gustafsson K., Leguern C., Hirsch
                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                     precursor.
Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                             SLA class II
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Proc. Natl. Acad. Sci. U.S.A. 78:569-573(1981).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
expression of
                                                              Sache D.H.,
                                                                                                                                                                                                       NCBI_TaxID=9823;
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PIR; C93922; L2MS.
HSSP; P01842; 2MCG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochemistry 12:5400-5416(1973).
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MEDLINE=74048693; Pu
                            "Class II genes of
                                                                                                                                            SEQUENCE FROM N.A.
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(Rel. 14, Last sequence update)
(Rel. 38, Last annotation update)
I histocompatibility antigen, DQ h
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11254 MW;
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ProDm; PD000328; MHC_II_beta; 1.
SMART; SM00407; IGC1; 1.
PROSITE; PS50835; IG_LIKE; 1.
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SEQUENCE
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01-DEC-1992 (Rel. 24, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Carcinoembryonic antigen-related cell adhesion molecule 5
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SEQUENCE FROM N.A.
MEDLINE=90258861; PubMed=2342461;
Schrewe H., Thompson J., Bona M., Hefta L.J.F., Maruy
Hassauer M., Shively J.E., von Kleist S., Zimmermann
                                                                                                                                                                                                                                                                                                                                                                                    P06731;
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR000353; MHC_II_beta.
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Pred. No. 0.
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EXTRACELLULAR BETA-1.
EXTRACELLULAR BETA-2.
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                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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Genew;

HGNC:1817;

CEACAM5

; -; NOT_ANNOTATED_CDS.
); -; NOT_ANNOTATED_CDS.
); AAAS1967.1; -.
); CAA34474.1; -.

GO:0005887;

C:integral to 7110; Ig-like.

plasma membrane;

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EMBL; M17303; AAB59513.1; --
EMBL; M59265; AAA62835.1; JU
EMBL; M59256; AAA62835.1; JU
EMBL; M59256; AAA62835.1; JU
EMBL; M59257; AAA62835.1; JU
EMBL; M59258; AAA62835.1; JU
EMBL; M59259; AAA62835.1; JU
EMBL; M59260; AAA62835.1; JU
EMBL; M59709; -; NOT_ANNOTA;
EMBL; M5940; AAA51967.1; --
EMBL; M16042; AAA51963.1; --
EMBL; M16042; AAA51963.1; --
EMBL; M16042; AAA51972.1; --
EMBL; M16043; AAA61972.1; --
EMBL; M1604; AAA61972.1; --
EMBL; M1604; AAA61972.1; --
EMBL; M1604; AAA619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-89122014; PubMed=3220478;
Barnett T., Goebel S.J., Nothdurft M.A., Elting J.J.;
Barnett T., Goebel S.J., Nothdurft M.A., Elting J.J.;
Characinoembryonic antigen family: characterization of cDNAs coding for NCA and CEA and suggestion of nonrandom sequence variation in their conserved loop-domains.";
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Proc. Natl. Acad. Sci.
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"Primary structure of human carcinoembryonic antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beauchemin N., Benchimol S., Cournoyer D., Fuks A., Stanners C. "Isolation and characterization of full-length functional cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression.";
Mol. Cell. Biol. 10:2738-2748(1990)
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SIMILARITY: Belongs to the immunoglobulin superfamily.
SIMILARITY: Contains 7 immunoglobulin-like domains.
DATABASE: NAME-PROW; NOTE=CD guide CD66e entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd66e.htm".
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to H., Kosaki G.;
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JSITE; PS50835; IG_LIKE; 6.

""moglobulin domain; Glycoprotein; Limoglobulin domain; Glycoprotein; Limoglobulin domain; Repeat; 3D-structure
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KLHQEVNLVVMRATQLQKNLTCE - -
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                                                SSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTG
                                                                                                NQKKV-EFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVE-KLTGSGELWWQAERAS
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MEDLINE=70166723; PubMed=4909564;
Titani K., Wikler M., Shinoda T., Put
"The amino acid sequence of a lambda
complete amino acid sequence and the
                                                          "Structural rule of antibodies. Primary structure of immunoglobulin-L-chain of the lambda type, subgroup I protein Kern). V. The complete amino acid sequence ar interpretation.";
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MEDLINE=69088380; PubMed=4883841;
Milstein C., Clegg J.B., Jarvis J
"Immunoglobulin lambda-chains. Th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
   Hoppe-Seyler'в
[5]
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MEDLINE=83186114; PubMed=6404900;
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IGLC1 AND IGLC2 AND
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110:631-652(1968).
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EMBL; L38562; AAB35581.1;
EMBL; X51754; CAB38569.1;
EMBL; X51755; CAA330049.1;
EMBL; X51755; CAA36051.1;
                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
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MEDLINE=95255298; PubMed=7737190;
Stoppini M., Bellotti V., Negri A.,
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MEDLINE-82080680; PubMed-6273747;
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MEDLINE-90133913; PubMed-2515285;
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MEDLINE=75046825; PubMed=4215080;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 294:536-540(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Mol. Biol. 210:601-615(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PARTIAL SEQUENCE (BENCE-JONES PROTEIN MCG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Poljak R.J., Amzel L.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Characterization of the two unique immunoglobulins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=74109253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 n man.
                                                                                                                                                                                                                                                                                                                                                                                                                                             MISCELLANBOUS: The sequence shown is the Kern-/Oz-/Mcg- chain found in proteins SH, X, and NIG-64. The Kern protein has the Kern+ marker, the NEWM protein has the Oz+ marker, the Mcg protein has the Kern+ marker, and the Mcg+ marker.

MISCELLANBOUS: Six tandem lambda-type genes were identified and the 3 most 5' were sequenced. These correspond to the Mcg sequence the 3 most 5' were sequenced. These correspond to the Mcg sequence (lambda-1), the Kern-/Oz- sequence (lambda-2) and the Kern-/Oz-
                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                           equence.
                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE (MYELOMA PROTEIN NEWM).=74109253; PubMed=4814727;
L., Poljak R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                        (lambda-3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228:886-893 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Avey
                                                 ALT_INIT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Edmundson A.B.; light chain dimer crystallized of a molecule in two crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen B.L., Phizackerley R.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Merlini G., Garver F., Ferri G.; human anti-flavin monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       evolution of domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    light chain of a human myeloma
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Schiffer M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OF NEWM
                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of a
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region ger
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Kern-/Oz+
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RESULT 7

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STANDARD;

PRT;

105

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SCCSBABBAB

LAC PIG STANDA
PO1846;
21-JUL-1986 (Rel. 01,
21-JUL-1986 (Rel. 01,
10-OCT-2003 (Rel. 42,
1g lambda chain C reg
Sus scrofa (Pig).
Eukaryota; Metazoa; C
Mammalia; Eutheria; C
NCBI_TaxID=9823;

. 01, Last . 42, Last C region.

sequence up

on update)

Cetartiodactyla; Chordata;

Craniata; Vertebrata; actyla; Suina; Suidae;

Euteleostomi; Sus.

42,

Created)

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Matches
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                                                                                    SEQUENCE
                                                                                                                                                                                 STRAND
                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 1.
SMART; SM00407; IGc1; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                Genew; HGNC:5856; Genew; HGNC:5857;
                                                                                                                                                                                               VARIANT
                                                                                                                                                                                                              VARIANT
                                                                                                                                                                                                                           VARIANT
                                                                                                                                                                                                                                         VARIANT
                                                                                                                                                                                                                                                                                                                                     InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                          GO; GO:0003823; F:antigen binding; GO; GO:0006955; P:immune response;
                                                                                                                                                                                                                                                                                                                                                                                              Genew; HGNC:5855;
                                                                                                                                                                                                                                                       VARIANT
                                                                                                                                                                           超LIX
                                                                                                                                                                                                                                                                                                 mmunoglobulin domain; Immunoglobulin C
                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                    ; 2MCG; 15-JUL-92.
; 7FAB; 31-JAN-94.
; 1AQK; 04-FEB-98.
; 1LIL; 15-MAY-97.
             579
61
                            \vdash
                                                              Similarity
             SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 609
                                        QPR-EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP-ENNYKTTPPVLD
SNNKYAASSYLSLTPEQWKSHRSYSCQVTHE
                            QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQ
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IGLC2.
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                                                        18;
                                                                                                                                                                                                            A -> N (IN MCG+ MARKER).
/FTId=VAR 003898.
S -> T (IN MCG+ MARKER).
/FTId=VAR 003899
S -> G (IN KERN+ MARKER).
/FTId=VAR 003900.
T -> K (IN MCG+ MARKER).
                                                              Score 159; D
                                                       Pred. No. 0.00
3; Mismatches
                                                                                                                                                                                                                                                              INTERCHAIN
                                                                                                                                                                                              /FTId=VAR_003901.
R -> K (IN OZ+ MARKER).
                                                                                                                                                                                        FTId=VAR_003902
                                                                                    DCD9C7C201C13CC2 CRC64;
                                                                                                                                                                                                                                                                                                  region; Bence-Jones protein;
                                                                                                                                                                                                                                                               HTIW)
91
                                                                      DB 1;
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                                                                    Length 105;
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EXERGENCE SERVICE SERVICES SER
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Best Local
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NON TER 1
DOMAIN 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHICK
CHICK STANDARD; PRT; 1906 AA.
P11799; P19038;
01-OCT-1989 (Rel. 12, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Myosin light chain kinase, smooth muscle and
(EC 2.7.1.117) (MLCK) [Contains: Telokin].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE.
                                                                                                                                                                                                                                                                       "Multiple gene products are produced transcription region."; FEBS Lett. 373:217-220(1995).
                   SEQUENCE OF 649-1906 FROM N.A., TISSUE=Fibroblast;
                                                                                        Proc.
                                                                                                              Olson N.J., Pearson R.B., Needleman D.S., Hur
Means A.R.;
"Regulatory and structural motifs of chicken
chain kinase.";
                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM MLCK-
MEDLINE=90192792; PubMed=2315320;
                                                                                                                                                                                                                                                                                                                                          Watterson D.M., Collinge M., Lukas T.J., Stepanova O.V., Shirinsky V.P.;
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM MLCK-210).
MEDLINE=96033976; PubMed=7589469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EC 2.7.1.117) (MLCK) [Contains: Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig; 1.
SMART; SM00407; IGc1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A02129; L1PG.
HSSP; P01842; 2MCG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunoglobulin lambda chains.";
Biochemistry 16:3765-3772(1977)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Amino acid sequence of normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISCELLANEOUS: This chain was obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS50835; IG_LIKE; 1.
PS00290; IG_MHC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QPKAAPTVNLFPPSSEELGTNKATLVCLISDFYPGAVTVTWKAGGTTVTQGVETTKPSKQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                        Sci.
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PubMed=2202734;
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86
104
                                                                                                                                                                                                                            (ISOFORM MLCK-108).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.6%;
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                                                                                      U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 156; DB
Pred. No. 0.00
L5; Mismatches
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3817AAEBD747C396 CRC64;
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                                                                                        87:2284-2288(1990)
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                                             AND
                                           PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                         from
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                                                                                                                                                                                                                                                                                                                                                                  van
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                                                                                                                                                                                                                                                                                                                       a novel
                                                                                                                                                                              Hurwitz M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from a mixture
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                                                                                                                                   gizzard
                                                                                                                                                                                                                                                                                                                                                               Eldik L.J., Birukov K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   non-muscle
                                                                                                                                                                                                                                                                                                                    protein kinase
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EMBL; X52876; CAA370; EMBL; M31048; AAA490; EMBL; M14953; AAA490; EMBL; M96655; AAA490; EMBL; M88283; AAA486; EMBL; M88284; AAB537; PIR; S68235; S68235. PDB; 1CDL; 31-AUG-94 PDB; 1VRK; 27-APR-99 InterPro; IPRO08957;

InterPro;

IPR008957; IPR003961; 31-AUG-94. 27-APR-99.

FN_III-like. FN_III. Ig-like.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shoemaker M.O., Lau W., Shattuck R.L., Kwiatkowski A.P., Matrislan P.E., Guerra-Santos L., Wilson E., Lukas T.J., van Eldik L.J., Watterson D.M.; "Use of DNA sequence and mutant analyses and antisense oligodeoxynucleotides to examine the molecular basis of nonmuscle myosin light chain kinase autoinhibition, calmodulin recognition,
                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collinge M., Matrisian P.E., Zimmer W.E., Shattuck R.L., Lukas T. van Eldik L.J., Watterson D.M.;
"Structure and expression of a calcium-binding protein gene conta within a calmodulin-regulated protein kinase gene.";
within a calmodulin-regulated protein kinase gene.";
Mol. Cell. Biol. 12:239-2371(1992).
-I- FUNCTION: Phosphorylates a specific serine in the N-terminus myosin light chain, which leads to the formation calmodulin/M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=87157587; PubMed=3030394;
Guerriero V. Jr., Russo M.A., Olson N.J., Putkey J.A., Mean "Domain organization of the chain "Domain organization of "Domain organization" "."
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"Molecular cloning of the chicken gizzard telokin "Molecular cloning of the chicken gizzard telokin rank Riochem. Biophys. 299:242-247(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            deduced from a cloned cDNA.";
Biochemistry 25:8372-8381(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1750-1906 FROM N.A. (ISOFORM TELOKIN)
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                                                                                                                                                                                                                                                                                                                                                                                           GIZZARD.

DOMAIN: TELOKIN BINDS CALMODULIN.

DOMAIN: TELOKIN BINDS CALMODULIN.

SIMILARITY: Belongs to the Ser/Thr family of protein kinase

SIMILARITY: Contains 9 immunoglobulin-like C2-type domains.

SIMILARITY: Contains 1 fibronectin type III domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY: ISOFORM TELOKIN IS EXPRESSED IN GIZZARD HEART, LUNG, INTESTINE, AND SKELETAL MUSCLE ALTHOUGH THE LETTEE EXPRESSION IN THE LATTER WERE MUCH LESS THAN THAT IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          signal transduction complexes which allow selective
of calcium signals.
CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADE
                                                                                               X52876; CAA37056.1;

X52876; CAA37057.1;

X52876; CAA37058.1;

X52876; CAA37058.1;

M31048; AAA49069.1;

M44953; AAA69964.1;

M96655; AAA49081.1;

M96655; AAA49081.1;

M88283; AAA48647.1;

M88284; AAB53768.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         light-chain] phosphate.
ALTERNATIVE PRODUCTS:
Event-Alternative initiation;
Comment=At least 3 isoforms,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MLCK-108/Smooth-muscle and
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Query Match
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Matches 149
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R InterPro; IPR002290; Ser_thr_pkinase.

R InterPro; IPR002290; Ser_thr_pkinase.

R Pfam; pP00041; fn3; 1.

R Pfam; pP00047; ig; 9.

Pfam; pP00069; pkinase; 1.

R Pfam; pP00060; PN3; 1.

R ProDom; pD000001; Prot kinase; 1.

R SMART; SM00060; FN3; 1.

R SMART; SM00020; S_TKC; 1.

R SMART; SM00220; S_TKC; 1.

R SMART; SM00220; S_TKC; 1.

R R SMART; SM00220; S_TKC; 1.

R R SMART; SM00107; PROTEIN KINASE_ATP; 1.

PROSITE; PS00107; PROTEIN KINASE_ST; 1.

R PROSITE; PS00108; PROTEIN KINASE_ST; 1.
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FOR ISOFORM TELOKIN.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 7.
IG-LIKE C2-TYPE 8.
FIBRONECTIN TYPE-III.
                                                                                  POLY-GLU.
PHOSPHORYLATION.
PHOSPHORYLATION.
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MW; AD7D8A3B69EE3363
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IIB-1.
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IIB-3
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                                   Score 155;
Pred. No. 0.
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S C2-TYPE 9.

Y SIMILARITY).

Y SIMILARITY).
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CARBOHYD
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GO; GO:0003823; F:antigen binding;
GO; GO:0006955; P:immune response;
InterPro; IPR0077110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003506; Ig_MHC.
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SMART; SM00407; IGc1; 3.
PROSITE; PS50835; IG_LIKE;
PROSITE; PS00290; IG_MHC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Okuyama T., Munekata E.; "Amino acid sequence of hinge region of a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Primary structure of the Fc region of human immunoglobulin D: implications for evolutionary origin and biological function."; Proc. Natl. Acad. Sci. U.S.A. 78:504-508(1981).
                                                                                                                                                                                CARBOHYD
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AQASSVPTAQPQAEGSLAKATTAPATTRNTGRGGEEKKKEKEEQEERETKTPECPSHT
                                   QSQPQRTFPEIQRRDSYYMTSSQLSTPLQQWRQG-EYKCVVQHTASKSKKEIFRWPESPK
                                                       EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN----
                                                                         PTKAPD-----VFPIISGCRHPKD-----NSPVVLACLI-TGYHPTSVTVTWYM-GT
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O-LINKED (POTENTIAL).
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N-LINKED (GLCNAC. . .).
N-LINKED (GLCNAC. . .).
M-, DALDE73519C76C1D CRC64;
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Pred. No. 0.00
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IG-LIKE 2.
IG-LIKE 3.
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105:1066-1071(1982)
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                                                                                                                          RESULT 79
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=88196070; PubMed=3129289;
MEDLINE=88196070; P.A., Kindt T.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mami F., Cazenave P.A., Kindt T.J., "Conservation of the immunoglobulin EMBO J. 7:117-122(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1991 (Rel. 17, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
Ig lambda-5 chain C region
Mus spretus (Western wild mouse).
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01-FEB-1991
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HSSP; P01842; 2MCG.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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Pfam; PF00047; 1g; 1.

SMART; SM00407; IGc1; 1.

PROSITE; PS50935; IG LIKE; 1.

PROSITE; PS00290; IG MHC; FALSE NEG.

PROSITE; PS00290; IG MHC; FALSE NEG.

Temporalobulin domain; Immunoglobulin C
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SEQUENCE
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Oryctolagus cuniculus (Rabbit).
Oryctolagus Cuniculus (Chordata; C
                                                                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN-Basiles;
Heidmann O., Rougeon F.;
Heidmann O., Rougeon F.;
"Multiplicity of constant kappa light chain genome: a b4b4 homozygous rabbit contains a EMBO J. 2:437-441(1983).

-I- MISCELLANEOUS: In Basilea rabbits, the miscellaneous contains a contained by the contained by the miscellaneous contained by the contained by 
                                                                     This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus
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-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02130; L/RB.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Garcia I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Ci
Mammalia; Eutheria; Lagomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The primary structure of the communoglobulin lambda-chains."; Biochem. J. 197:177-183(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=82091105; PubMed=6797414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5-MAR-2004
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                                                                                                                             is lambda. The kappa chain shown is a minor rabbit B allotypes have Cys-64. SIMILARITY: Contains 1 immunoglobulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISCELLANEOUS: This lambda chain expresses the c7 allotypic
SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        584
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IPR003597; Ig_cl.
IPR003006; Ig_MHC.
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105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cuniculus (Rabbit).
Metazoa; Chordata; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 43, Last annotation updat
chain C region.
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86
104 I
11484 MW;
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32.7%;
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Pred. No. 0.0017;
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a; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B427513272E8663D CRC64;
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                                                                                                                                                                                                       the major type of light
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                                                                                                                                                                                                                                                                                                  genes in the rabbit kappa-bas gene.";
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                                                                                                                                        domain.
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      restrictions
                                                                  a collaboration
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outstation -
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RESULT
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Best Local S
Matches 31
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NON TER 1
DOMAIN 6
DISULFID 27
DISULFID 106
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SMART; SM00407; IGc1; 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00290; IG MHC; FALSE NEG.
Immunoglobulin domain; Immunoglobulin
                                                       STRAIN=129; TISSUE=Embryo;
MEDLINE=94117008; PubMed=7507076;
Cybulaky M.I., Allan-Motamed M., Collins
"Structure of the murine VCAM1 gene.";
                                                                                                                                                                                      TISSUE=Lymph node;
MEDLINE=93246254; PubMed=7683304;
Araki M., Araki K., Vassalli P.;
"Cloning and sequencing of mouse \text{V}
Gene 126:261-264(1993).
                                                                                                                                                                                                                                                                                                                                                         Hession C., Moy P., Tizard R., Chish
Burkly L., Miyake K., Kincade P., Lo
"Cloning of murine and rat vascular
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EMBL; V00885; -; NOT_ANNOTATED_CDS
PIR; A02121; K4RBBS.
                                                                                                                                                                                                                                                                                                                                              Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN=FVB; TISSUE-Lung;
MEDLINE=92181437; PubMed=1371918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1993 (Rel. 25, C
01-APR-1993 (Rel. 25, I
10-OCT-2003 (Rel. 42, I
Vascular cell adhesion
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SEQUENCE
                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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                                          18:387-391(1993).
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OF 1-693
                                                                                                                                                                                                                                                                                                                                          Biophys.
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106
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25, Last sequence update)
42, Last annotation update)
FROM
                                                                                                                                                                                                                                                                                                                                          Res.
                                                                                                                                                 (ISOFORM
                                                                                                                                                                                                                                                                                                    (ISOFORM
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N.A.
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(ISOFORM
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Pred. No. 0.0017;
9; Mismatches 3(
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Sciurognathi; Muridae;
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                                                                                                                                                                                                               VCAM-1 cDNA.";
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                                                                                                                                                                                                                                                                                                                                                                                                          Williams
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EMBL; M84487; EMBL; L22355; EMBL; L22301; EMBL; L22301; EMBL; L22350; EMBL; L22350; EMBL; L22351; EMBL; L22353; EMBL; L22353; EMBL; L22353; EMBL; L22353; EMBL; L22353; EMBL; L22354; EMBL; EMBL; L22354; EMBL; EMBL
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SEQUENCE FROM N.A. (ISOFORM 2).
STRAIN=C57BL/6; TISSUE=Liver;
MEDLINE=95015899; PubMed=7523515;
Kumar A.G., Dai X.Y., Kozak C.A.,
Ballantyne C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KOTENAGA R., ANGO J., TSUDOI H., KAMIYA A.;
SUDMILTEG (DEC-1995) TO THE EMBL/GENBANK/DDBJ databases.
SUDMILTEG (DEC-1995) TO THE CELL RECOGNITION. APPEARS TO FUNCTION IN LEUKOCYTE-ENDOTHELIAL CELL ADHESION. INTERACTS WITH THE BETA-1
INTEGRIN VLA4 ON LEUKOCYTES, AND MEDIATES BOTH ADHESION AND SIGNAL
TRANSDUCTION. THE VCAMI/VLA4 INTERACTION MAY PLAY A
PATHOPHYSIOLOGIC ROLE BOTH IN IMMURE RESPONSES AND IN LEUKOCYTE
EMIGRATION TO SITES OF INFLAMMATION.

POSTBLELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (LONG ISOFORM) OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Terry R.W., Kwee L., Levine J.F., Labow M.A.; "Cytokine induction of an alternatively spliced murine vascular cell adhesion molecule (VCAM) mRNA encoding a glycosylphosphatidylinositol-anchored VCAM protein."; Proc. Natl. Acad. Sci. U.S.A. 90:5919-5923(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=FVB/N; TISSUE=Kidney; MEDLINE=93317595; PubMed=7687058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-93232042; PubMed-7682556;
Moy P., Lobb R., Tizard R., Olson D., Hession C.;
"Cloning of an inflammation-specific phosphatidyl form of murine vascular cell adhesion molecule-1."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM STRAIN-FVB; TISSUE-Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=NIH Swiss, and 129/Sv;
Kumar A.G., Dai Y.X., Kozak C.A., Mims M.P., Gotto A.M.
Ballantyne C.M.,
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 311-345 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTM: The GPI-anchor is located on position 319 of isoform 2 SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=2; Synonyma=Short;
IsoId=P29533-2; Sequence=VSP_002581, VSP_002582;
TISSUE SPECIFICITY: Expressed on inflamed vascular endothelium, as
well as on macrophage-like and dendritic cell types in both normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR ALTERNATIVE PRODUCTS:
EVENt-Alternative splicing; Named isoform Name=1; Synonyms=Long;
IsoId=P29533-1; Sequence=Displayed;
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l. 153:4088-4098(1994).
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                                            268:8835-8841(1993).
    L1; JOINED.
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CHAIN 25 739 VASCULAR CELL ADHESION DOMAIN 25 698 EXTRACELLULAR (POTENTI) TRANSMEM 699 720 POTENTIAL.
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PIR; B48919; A46052.
PIR; JN0581; JN0581.
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PRINTS; PRO1474; VCAM1.
SMART; SM00408; IGC2; 3.
PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003598; Ig_c2.
InterPro; IPR003989; VCAM-1.
Pfam; PF00047; ig; 5.
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InterPro; IPR003987; ICAM VCAM-1.
InterPro; IPR007110; Ig-11ke.
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L; L22349; AAA16920.1;
L; L122349; AAA16920.1;
U12878; AAB60660.1;
U12880; AAB60660.1;
L; U12887; AAB60660.1;
L; U12887; AAB60664.1;
U12887; AAB60664.1;
L; U12887; AAB60064.1;
L; U12887; AAA80010.1;
L; U12882; AAA80011.1;
L; U12882; AAA80011.1;
L; U12876; AAA80011.1;
L; U12876; AAA80011.1;
L; U12876; AAA80015.1;
L; U12877; AAA80015.1;
L; U12878; AAA80016.1;
L; U12878; AAA80016.1;
L; U12879; AAA80016.1;
L; U12841; AAA69546.1;
L; U12841; AAA69546.1;
L; U12541; AAA69576.1;
L; U12541; U12541; AA
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                                                                   Similarity
KKGDTVELTCTASQKKSIQFHW--KNSNQI-KILGNQGSFLTKGPSKLNDRADSRRSLWD
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IG-LIKE C2-TYPE 1.
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EKPFIVDISPGSQVAAQVGDSVVLTCAAIGCDSPSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-OCT-2003 (Rel. 01, Last sequence update)
19 kappa chain C region, A allele.
Rattus norvegicus (Rat).
Eukarrora.
                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig c1.
InterPro; IPR00306; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
Pfam; PP00047; Ig; 1.
SMART; SM00407; IGc1; 1.
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PROSITE; PS00290; IG_MHC; 1.
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HSSP; P01842; 2MCG.
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Mammalia; Eutheria;
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PTVSIFPPSMEQLTSGGATVVCFVNNFYPRDISVKWKIDGSEQRD-----GVLDSVTDQD
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                                                                                          4.4%;
llarity 31.5%;
Conservative 2
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(Rel. 01, Last seq
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106
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Rodentia;
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                                                                                          Score 150; DB 1;
Pred. No. 0.0027;
3; Mismatches 20
                                                                                                                                                                                  INTERCHAIN (WITH A HEAVY CHAIN)
B7E120D9700DDD66 CRC64;
                                                                                                                                                                                                                                                        IG-LIKE
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Sciurognathi;
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1997710; 008951; 070426; 090WI5;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Create
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-419 FROM N.A., AND TISSUE SPECI
STRAIN-WAG/Rij; TISSUE=Alveolar macrophage;
MEDLINE=98375871; PubMed=971203;
Adams S., van der Laan L.J.W., Vernon-Wilson
Renardel de Lavalette C., Doepp E.A., Dijkstr
                                                                                                                   MEDLINE=98008865; PubMed=9344856; Ochi F., Matozaki T., Noguchi T., Fujioka Y., Yamao T., Takada T., Takada H., Pukunaga K., Okabayashi Y., Kasuga M.; Tspidermal growth factor stimulates the tyrosine phosphorylation of SHPS-1 and association of SHPS-1 with SHP-2, a SH2 domain-containing SHPS-1 and association of SHPS-1 with SHP-2, a SH2 domain-containing SHPS-1 and association of SHPS-1 with SHP-2, a SH2 domain-containing SHPS-1 and association of SHPS-1 with SHP-2, a SH2 domain-containing SHPS-1 and association of SHPS-1 with SHP-2, a SH2 domain-containing SHPS-1 and association of SHPS-1 with SHP-2, a SH2 domain-containing SHPS-1 and association of SHPS-1 with SHP-2, a SH2 domain-containing SHPS-1 and association of SHPS-1 with SHP-2, a SH2 domain-containing SHPS-1 with SHPS-1 with
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Ullu E., 1
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419-429; 446-467 AND 496-506, N-GLYCOSYLATION,
STRAIN=Fischer 344; TISSUB-Macrophage;
MEDLINE=98449911; PubMed=9774638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAILNESprague-Dawley; TISSUB-Brain;
MEDLINE=97415431; PubMed=2271230;
Sano S.-I. Ohnishi H. Omori A., Hasegawa J.,
"BIT, an immune antigen receptor-like molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., SEQUENCE OF 42-60; 68-91; 128-137; 150-158; 174-189; 192-202; 204-212; 218-237; 259-270; 279-282; 405-415 AND 446-453, N-GLYCOSYLATION, PHOSPHORYLATION ON TYROSINE RESIDUES, AND PERSONNEL OF TRANSPORT OF TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION IN RESPONSE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Signal-regulatory protein is selectively neuronal cells.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
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                                                                                  protein tyrosine phosphatase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        van den Berg T.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunol.
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putative receptor mediating the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. 16:6887-6899(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161:1853-1859(1998)
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                                                 Res.
                                                 Commun.
                                                                                                                                                                                                                                                                                                                                                                                                                EGF,
                                                 239:483-487 (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                      INTERACTION
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ND TISSUE
                                                                                                                                                    domain-containing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Simmons D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Solimena M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                      PTPN11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           405-417;
SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to mitogens
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Glycoprot
SIGNAL
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-I- FUNCTION: Immunoglobulin-like cell surface receptor for CD47. Acts as docking protein and induces translocation of PTPN6, PTPN1 and other binding partners from the cytosol to the plasma membrane. Supports adhesion of cerebellar neurons, neurite outgrowth and glial cell attachment. May play a key role in intracellular signaling during synaptogenesis and in synaptic function. Involved in the negative regulation of receptor tyrosine kinase-coupled cellular responses induced by cell adhesion, growth factors or insulin. Mediates negative regulation of phagocytosis, mast cell activation and dendritic cells and inhibits cytokine production by mature dendritic cells and inhibits cytokine production by mature dendritic cells. May play a role in the release of nitric oxide by macrophages (May similarity).

-I- SUBUNIT: Binds PTPN11 when tyrosine-phosphorylated, except in macrophages, where it primarily binds PTPN6. Binds GRB2 in vitro. Binds FGR. Binds JAK2 irrespective of its phosphorylation status and forms a stable complex. Binds FTPN6. Binds GRB2: The resulting complex recruits FYB. Binds PTX2B (By similarity).

-I- SUBCELULAR LOCATION: Type I membrane protein.

-I- TISSUE SPECIFICITY: Highly expressed in brain, spleen, lung, liver and kidney. Detected at lower levels in heart. Highly expressed in dendritic cells in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D85183; BAA12734.1; -.
EMBL; D38468; BAA20368.1; -.
EMBL; U62328; AAC68478.1; -.
EMBL; AF055065; AAC18089.1; -.
HSSP; P01703; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; ig; 3.
SMART; SM00407; IGc1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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MEDLINE=98204923; PubMed=9535915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takada T., Matozaki T., Takada H., Fukunaga K., Noguchi T.,
Fujioka Y., Okazaki I., Tsuda M., Yamao T., Ochi F., Kasuga M.;
"Roles of the complex formation of SHPS-1 with SHP-2 in
insulin-stimulated mitogen-activated protein kinase activation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Contains 2 immunoglobulin-like C1-type domains. SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dendritic cells
                                                                                                                                                                                                                                                                                                                                                                                                       PS50835; IG_LIKE; 3.
PS00290; IG_MHC; 1.
Signal; Transmenorane; Immunoglobulin domain; SH3-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-glycosylated. Phosphorylated on tyrosine residues in response to insulin, phosphorylated on tyrosine factors. Dephosphorylated by adhesion or epidermal growth factors.
         28
374
395
32
150
255
255
172
172
274
                                                                                                                                                                                                                                                                                                                                                                                              Phosphorylation.
      373
394
138
248
349
1229
2229
3329
                                                                                          POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE CY-TYPE.
IG-LIKE C1-TYPE 1.
IG-LIKE C1-TYPE 2.
POTENTIAL.
POTENTIAL.
SH2-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                       TYPE
                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL)
                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                       PROTEIN-TYROSINE PHOSPHATASE NON-RECEPTOR TYPE SUBSTRATE 1.
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426	126	374	92	314	32	259	ry Match t Local S ches 83	SEQUENCE	CONFLICT	CONFLICT	CONFLICT	CONFLICT	CONFLICT	CONFLICT	CONFLICT	CONFLICT	CONFLICT			MUTAGEN			MUTAGEN	HOLDON	MITTAGEN	MOTAGEN	CARBOHYD	CARBOHYD	CARBOHYD	CARBOHYD	CARBOHYD	CARBOHYD	CARBOHYD	CARBOHYD	CARBOHYD	MOD_RES	MOD_RES	MOD_RES	ï	SITE
PKDTLMISR:	QKGIVEPDTE	DSGQVLLESI	TNVSDATK-I	LVVMRATQLQKNLTCEVWGPT	: :	KEVSVKRVT	imilarit ; Conse	509 AA;	450	416 418	405)))))	189	1 99	5 U	10	80			501			477		460	416	345	320	293	271	242	209	181	93 169	54.4	477	460	436	501	446
PEVTCVVI	EIKSGGGTTLYVL	SNIK	RNIMD	QKNLTCEVWO	; ; ; QADKSVSVAAGDS	DD PKL QMGKI	4.4%; Y 21.6%; rvative 6	55690 MW	450	416 421	405	205	189	100	5 8 2 2	10	8			501			477	- 0	460	L	345	320	293	271	242	209	181	93 169	55 E	477	460	436	504	451 463
PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL 485		VLPTWSTPVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPK 425	FSICISNVTPEDAGTYYCVKF 125	SPKLMLSLKLENKEAKVSKREKPVWVLNE	DSATLNCTVSSLTPVGPIKWFKGEGQNRSPIYSFIGGEHFPRI 91	lpihltlpqalpqyagsgnltlaleaktgklhq	Score 150; DB 1; Length 509; Pred. No. 0.021; 53; Mismatches 158; Indels 80; Gaps 16;	; SBE1FE0A4DD429F4 CR	E (IN REF. 3; AA	-> EGON (IN REF.	G -> F (IN REF. 3; AA SEQUENCE).	L (IN REF. 3; AA	N (IN REF. 2).	MP (IN REF.	C (IN	MISSING (IN REF. 4).	ASSOCIATED WITH F-436, F-460 AND F-4//. P -> L (IN REF. 4).	AND PTPN11 BINDING;	TA ONA	8.5	1 BINDING;	NOTING ABOUTSHES TYPOSTNE	ES.	3.	60, F-477 AND F-501	NG; WHI		 	.:	 	.:_	 	(GLCNAC) (POTENTIAL)		C) (POTENTI	(FOIENTIAL). PHOSPHORYLATION (BY TYR-KINASES). DHOSPHORYLATION (BY TYP-KINASES).	PHOSPHORYLATION (BY TYR-KINASES)	PHOSPHORYLATION (BY TYR-KINASES)	BINDING (POTENTIAL).	SH3-BINDING (POTENTIAL). SH2-BINDING (POTENTIAL).

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RESULT 84
HB2C_PIG
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Pfam; PF00969; MHC II beta; 1.
ProDom; PD000328; MHC II beta; 1
SMART; SM00407; IGC1; II beta; 1
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00290; IG MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1990
01-APR-1990
15-JUL-1999
     TRANSMEM
DOMAIN
DISULFID
DISULFID
CARBOHYD
SEQUENCE
                                                                                    DOMAIN
DOMAIN
                                                                                                                                                     MHC II;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Class II genes of miniature swine. expression of two allelic class II D J. Immunol. 145:1946-1951(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
SLA class II histocompatibility antigen, DQ P
                                                                                                                                                                                                                                                                                                                                           EMBL; M31497; AAA31084.1; -. EMBL; M32117; AAA53110.1; -.
                                                                                                                                                                                                                                                                                                                  PIR; A60404; A60404.
HSSP; P13760; 2SEB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gustafsson K., Leguern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           precursor.
                                                                                                                                                                                                                                                         InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR000353; MHC_II_beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sache D.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90361905; PubMed=2391424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa (Pig).
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                                                                                                                                                                  Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF
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126
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230
251
261
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29550
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Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                   II_beta; 1.
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        3
                             CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
                                                                                  SLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DO HARLOTYPE C BETA CHAIN.
EXTRACELLULAR BETA-1.
EXTRACELLULAR BETA-2.
CONNECTING PEPTIDE.
                   N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
     AA9581F2A3B1969D CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . IV. Characterization DQB cDNA clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261
                   (GLCNAC
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Sus.
                   (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   270
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RESULT 85
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Best Local S
Matches 51
                                                                                               MEDLINE=20289799; PubMed=10830953;
Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
Rosenthal A., Kudoh J., Shibuya K., Kawassaki K., Asakawa S.,
Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
Scharfe M., Schoen O., Desario A., Reinelt J., Kauer G., Bloecker H.,
Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
Lehrach H., Reinhardt R., Yaspo M.-L.;
"The NNA servence of human chromome 3.1".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSCA HUMAN STANDARD;

060469; 060468;

16-0CT-2001 (Rel. 40, Created)

16-0CT-2001 (Rel. 40, Last seq

10-0CT-2003 (Rel. 42, Last ann
                                                         Nature 405:311-319(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN
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                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    Brain
                                                                                                                                                                                                                                                                                                                                                                  Agarwala K.L., Nakamura S., Tsutsumi y
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20384934; PubMed=10925149; Agarwala K.L., Nakamura S., Tsutsumi Y.,
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             nervous system."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "DSCAM: a novel member of the immunoglobulin superfamily maps 
Down syndrome region and is involved in the development of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamakawa K., Huot Y.-K., Ha
Lyons G.E., Korenberg J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98087574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSCAM
                                                                                     "The DNA sequence of human chromosome 21.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                  intercellular adhesion.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSCAM: a novel member
              NERVOUS SYSTEM DEVELOPMENT. SUBCELLULAR LOCATION: TYPE
                                            INDEPENDENT HOMOPHILIC BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            syndrome
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                                                                                                                                                                                                                                                                                                                                                                                                               FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | : : |:|:| | | | | | VLVMLEMNLQRGDVYTCRVEHSSLQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN-NYKTTPPVLDSDGSFFLYS
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                                                                                                                                                                                                                                                                                                                                      Brain Res.
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    Last sequence update)
    Last annotation update)

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SECRETED
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6; Mismatches
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              PROTEIN (PROBABLE).
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InterPro; IPR008957; FN_III-like.
InterPro; IPR003961; FN_III.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
Pfam; PF00041; fn3; 6.
Pfam; PF00047; ig; 9.
SMART; SM00060; FN3; 6.
SMART; SM00060; FN3; 6.
SMART; SM00408; IGc2; 7.
PROSITE; PS50835; IG_LIKE; 9.
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
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Transmembrane; Alternative splicing.
SIGNAL 1 17 POTENTIAL.
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Name=Short; Synonyms=CHD2-42;
IsoId=O60469-2; Sequence=VSP_002502, VSP_002503;
TISSUE SPECIFICITY: Primarily expressed in brain.
SIMILARITY: Contains 10 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 6 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO:0005887; C:integral to plasma membrane; TAS. GO:0005624; C:membrane fraction; TAS. GO:0007155; P:cell adhesion; TAS. GO:0007399; P:neurogenesis; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ween the Swiss Institute of Bioinforma
European Bioinformatics Institute. The
by non-profit institutions as long
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AF023449; AAC17966.1;
AF217525; AAF27525.1;
AL163283; CAB90464.1;
AL163281; CAB90436.1;
AL163281; CAB90444.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALTERNATIVE PRODUCTS:
Event=Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                 POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 4.

IG-LIKE C2-TYPE 5.

IG-LIKE C2-TYPE 7.

IG-LIKE C2-TYPE 8.

IG-LIKE C2-TYPE 8.

IG-LIKE C2-TYPE 9.

IG-LIKE C2-TYPE 11.

IG-LIKE C2-TYPE 10.

IG-LIKE C2-TYPE 11.

IG-LIKE C2-TYPE 10.

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                                  IARNEA -- AAVEHQSQLIVRVP -- PKFVVQPRDQDGIYGKAVILNCSAEG
                                                                KVSNKALPAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEW
                                                                                                                              DPEVKENWYVD
                                                                                                                                                             OLST--
                                                                                                                                                                                         TWSTPVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
                                                                                                                                                                                                                        KNSNLLPFNHRQVAFENNGTLKLSDVQKEV-----DEGEYTC
                                                                                                                                                                                                                                                        PTSPKLMLSLKL----ENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNIKVLP
                                                                                                                                                                                                                                                                                       GGVYRCTANNSAGVVLYQARINVRGPASIRPMKNITAIAGRDTYIHCRVIGYPYYSIKWY
                                                                                                                                                                                                                                                                                                                    AGSGNLTLALEAKTGKLHQEVNLVVMRATQLQKNLT------
                                                                                                                                                                                                                                                                                                                                                     SPAEPVSLMCNVKGTPLPTITWTLDDDPILKGGSHRISQMITSEGNVVSYLNISSSQVRD
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                                                                                               DLPITITWQKDGRPIPGSLGVTIDNI--
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Pred. No. 0.
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Missing (in isoform Short).
/FTId=VSP_002503.
HRPGDLIHLPPYLRMDFLINRGGPGTSRDLSLGQACLEPQK
SRTLKRPTVLEPIPMEAASSASSTREGQSWQPGAVATLPQR
EGAELGQAAKMSSSQESLLDSRGHLKGNNPYAKSYTLV ->
IGQVTSYICLHTLEWTPC (IN REF. 1).
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RESULT 86
    Hilschmann N., Barnikol H.U., Hess M., Steinmetz-Kayne M., Suter L., Watanabe (In) Franck F., Shugar D. (eds.);
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Hieter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr.,
"Cloned human and mouse kappa immunoglobulin constant
genes conserve homology in functional segments.";
Cell 22:197-207(1980).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE (MYELOMA PROTEIN EU).
MEDILINE-71064023; PubMede-5489770;
Gottlieb P.D., Cunningham B.A., Rut
"The covalent structure of a human
acid sequence of the light chain.";
Biochemistry 9:3155-3161(1970).
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P01834;
                                                                          Titani K., Shinoda T., Putnam F.W.;
"The amino acid sequence of a kappa type Bence-Jones protein. 3.
complete sequence and the location of the disulfide bridges.";
J. Biol. Chem. 244:3550-3560(1969).
                                                                                                                     SEQUENCE (BENCE-JONES PROTEIN AG).
MEDLINE-69234734; PubMed-4893682;
Titani K., Shinoda T., Putnam F.W.
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"The covalent structure of a human Intrachain disulfide bonds.";
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21-JUL-1986 (Rel. 01, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Ig kappa chain C region.
               MEDLINE=70201507; PubMed=5447531;
Kohler H., Shimizu A., Paul C., P
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MEDLINE=68242259; PubMed=5586923;
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MEDLINE=72188439; PubMed=5027703;
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                                                                                                                                                                                  Hoppe-Seyler's
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                 Putnam F.W.;
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an gamma G-immunoglobulin. VI.
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sequence of light and heavy
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SWART; SW00407; IGc1; 1.
SWART; SW00407; IGc1; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MIC; 1.
Immunoglobulin domain; Immuno
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"Extended analysis of AL-amyloid protein from abdominal wall subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";
Biochem. Biophys. Res. Commun. 245:713-716(1998).
-i- MISCELLANBOUS: The EU sequence has the INV (3) allotypic marker, 45-Ala and 83-Val. The ROY sequence has the INV (1,2) allotypic marker, 45-Ala and 83-Leu.
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DISULFID
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InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MIM; 147200; -
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MEDLINE=98249779; PubMed=9588180;
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1D5I; 09-FEB-00.

1D6V; 04-OCT-00.

1HEZ; 18-JUL-03.

1HKZ; 12-MAR-97.

117Z; 08-AUG-01.

1MIM; 15-MAY-97.
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Pred. No. 0.0036;
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InterPro; IPR008957; FN III-like.
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InterPro; IPR007110; Ig-like.
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InterPro; IPR003598; Ig_c2.
Pfam; PF00041; fn; 6.
Pfam; PF00047; ig; 4.
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                         European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in iffied and this statement is not removed. Usage by and for contitles requires a license agreement (See http://www.isb-sib.ch/arsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: IMPLICATED AS A TUMOR SUPPRESSOR GEN
SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
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SSSKSWITFD-LKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTL-----
                                                                                               EEQYNSTYRVVSVLTVLHQDWLNGKEYK-CKVSNK---ALPAPIEKTISKAKGQPREPQV
                                                                                                                                                                     ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
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                               YTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYS
                                                                                                                                   ----VF-FSREGDNRERALNTTQPGSLQLTVGNLKPEAMY---
------HAVSTS-----PTSILITWE--
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Pred. No. 0.11;
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10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel.
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Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L., Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Beaseley O.P., Bird C.P., Blates Y.S., Bridgeman A.M., Brown A.J., Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Cheg Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.P., Colgg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
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P78324; O00683;
Q9Y4U9;
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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MEDLINE=98143722; PubMed=9485180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97215901; PubMed=9062191; Kharitonenkov A., Chen Z., Sures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Placenta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fujioka Y., Kasug
"Mouse and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97223399; PubMed=9070220;
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                                                                                                                                                                                                            PubMed=11780052;
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ND VAL-131.
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ND INTERACTIONS
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DR MYD1 OR BIT OR MFR.
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LEU-96; ASN-100; ARG-107; GLY
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Q8TAL8; Q9H0Z2;
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TISSUE-Brain, Kidney, and Skin;

X MEDLINE-22388257; PubMede12477932;

X MEDLINE-22388257; PubMede12477932;

X Klausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Klausherg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

X Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

X Stapleton M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,

X Stapleton M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,

X Stapleton M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,

X Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

X Richards S., Morley K.C., Hale S., Garcia A.M., Gunaratne P.H.,

X Richards S., Worley K.C., Hale S., Garcia A.M., Gy L.J., Hulyk S.W.,

X Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

X Willalon D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

X Willalon D.K., Touchman J.W., Green E.D., Dickson M.C.,

X Butterfield Y.S.N., Touchman J.W., Green E.D., Dickson M.C.,

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A Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
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A Lehvaslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
A Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
A Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
A Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
A Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramaay H.,
A Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramaay H.,
A Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramaay H.,
A Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramaay H.,
A Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Shownkeen R., Sims S.,
A Swann R.M., Sycamore N., Soderlund C., Steward C.A., Sulston J.E.,
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A Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
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Delegoesse G., Sarfati M.;

"Bidirectional negative regulation of human T and dendritic of
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"Bidirectional negative regulation of human T and dendrition of dendri "SHPS-1 is a scaffold for assembling distinct multi-protein complexes in macrophages."; Curr. Biol. 9:927-930(1999). FUNCTION, AND INTERACTIONS WITH FYB; SCAP2
MEDLINE=99401000; PubMed=10469599;
Timms J.F., Swanson K.D., Marie-Cardine A.,
Schraven B., Neel B.G.; GLY-109 AND VAL-131. Gratham Maliszewski C., MEDLINE=21400825; FUNCTION, Latour S., PHOSPHORYLATION BY JAK2, AND INTERACTIONS WITH I activation: I activation of the FUNCTION: Immunoglobulin-like cell surface rece FUNCTION: Immunoglobulin-like cell surface rece translocation of the cortosol to the Natl. Acad. NA sequence and com 414:865-871(2001). S., H ARG-54; ALA-57; GLY-AND 400825; PubMed=11509594;
Tanaka H., Demeure C., Mateo V.,
C., Lindberg F.P., Oldenborg A. INTERACTION WITH Griffiths Lindberg F.P., Sarfati M.; comparative U.S.A. GLY-75; <u>.</u> Griffiths M.N.D., 99:16899-16903 (2002) AND 2), F ; ASP-95; CD47. analysis of human chromosome 20."; Ξ. ., Ullrich A., receptor/JAK2 AND VARIANTS LEU-44; ; LEU-96; ASN-100; ARC AND Rubio M., Ullrich Raab adhesion-regulated Gwilliam R. receptor to on of PTPN6, PTPN11 **.** Α. signaling Rudd Carter-Su AND JAK2 Brown for CD47. fullahy S.J., ratne P.H., Hulyk S.W., ARG-107; ņ dendritic Sanchez A. Hall PTPN11 , M Ħ THR-50 cells . . à. ₽.¤. T.E.,

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Matches
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Best Local (
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-i- ALTERNATIVE PRODUCTS:
Event-Alternation
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D86043; BAA12974.1; -.
EMBL; Y10375; CAA714403.1; -.
EMBL; Y10375; CAA71444.1; ALT_INIT.
EMBL; AB023430; BAA87929.1; -.
EMBL; AB023430; BAA87929.1; -.
EMBL; AL034562; CAB38874.1; -.
EMBL; AL034562; CAB38874.1; -.
EMBL; AL049534; CAB4662.1; ALT_SEQ.
EMBL; AL117335; CAC12723.1; -.
EMBL; BC033092; AAH33092.1; -.
EMBL; BC033092; AAH33092.1; -.
EMBL; BC0338510; AAH38510.1; -.
PIR; JC5287; JC5287.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ween the Swiss Institute of Bioinf European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Contains 2 immunoglobulin-like C1-type domains. SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTM: Phosphorylated on tyrosine residues stimulation with EGF, growth hormone, ins Dephosphorylated by PTPN11.
SIMILARITY: Contains 2 immunoglobulin-lik
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TISSUE SPECIFICITY: Ubiquitous. Highly expressed in brain.
Detected on myeloid cells, but not T cells. Detected at lower levels in heart, placenta, lung, testis, ovary, colon, liver, small intestine, prostate, spleen, kidney, skeletal muscle an
                                                                                                                                                                                                                                                                                                                                                              GO:0005886; C:plasma membrane; TAS
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Note=No experimental confirmation available;
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                                                     NLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLL
                                                                                                                 EELQVIQPDKSVSVAAGESAILHCTVTSLIPVGPIQWFRGAGPARELIYNQKEGHF----
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Pred. No. 0.
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in and PDGF.
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                                                                                                               RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., Almeida J.P., Babbage A.K., Bagguley C.L., RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Bealey O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Claek D., Clark S.Y., Clee C.M., Chapman J.C., Clamp M., Clark G.Y., Connor R.E., Corrby N.R., Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corrby N.R., RA Chapman J.C., Griffiths G., Giffiths M.N.D., Gwilliam R., Hall R.E., RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., RA Hammond S., Harley J.L., Kinghts A., Laird G.K., Lawlor S., RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., RA Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A., Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., RA Milne S.A., Mistry D., Woore M.J.F., Mullikin J.C., Nickerson T., RA Phillimore B.J.C.T., Patchalingam S.R., Plumb R.W., Ramsay H., RA Rice C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., RA Suann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A., Whitehead S.L., Whittaker P., Willey D.L., Williams S.A., Whitehead S.L., Whittaker P., Willey D.L., Williams S.A., Willey D.L., Williams S.A., Whitehead S.L., Whittaker P., Willey D.L., Williams S.A., Whitehead S.L., Whittaker P., Willey D.L., Williams S.A., RA Wilming L., Waray P.W., Hubbard T., Durbin R.M., Bentley D.R., Rack S.
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28-FEB-2003 (Rel
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                                Rogers J.
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Nature 414:865-871(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21638749; PubMed=11780052;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                sequence and comparative
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                                                                                                    P.W., Hubbard
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Chen Z., Sures
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                                   of human
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                                   chromosome 20.";
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RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,
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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,
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RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
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                                                                                Dietrich J., Cella M., Seiffert M., Buehring H.-J., Colonna M.; "Signal-regulatory protein beta 1 is a DAP12-associated activating receptor expressed in myeloid cells."; J. Immunol. 164:9-12 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tomasello E., Cant C., Buehring H.-J., Vely F., Andre P., Seiffert M
Ullrich A., Vivier E.,
"Association of signal-regulatory proteins beta with KARAP/DAP-12.",
Eur. J. Immunol. 30:2147-2156(200)).
                                                                  Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20072721; PubMed=10604985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=11169422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERACTION WITH TYROBP AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22388257;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERACTION WITH TYROBP,
GO:0005687; C:integral to plasma membrane; GO:0007166; P:cell surface receptor linked
                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Contains 2 immunoglobulin-like C1-type domain SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=000241-2; Sequence=VSP_007026;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Detected in monocytes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: Interacts with TYROBP. This interaction results in the recruitment of SYK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Immunoglobulin-like cell surface receptor involved the negative regulation of receptor tyrosine kinase-coupled signaling processes. Participates also in the recruitment of tyrosine kinase SYK.
                                                                                                                                                                                                                                                                                                                                                                                      PTM: N-glycosylated.
SIMILARITY: Contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Type I membrane
                                          603889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=000241-1; Sequence=Displayed;
                                                              HGNC:15928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-GLYCOSYLATION, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYK
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signal transdu.
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RESULT 90
SNE2_HUMAN
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Best Local S
Matches 57
                                                                                                           SNE2_HUMAN STANDARD; PRT; 6885 AA.

GBWXH0; QBNIS3; QBNF49; QBTER7; QBWWW3; QBWWW4; QBWWW5; QBWXH1;

QBWU50; QBUFQ4; Q9Y2L4, Q9Y4R1;

10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
Nesprin 2 (Nuclear envelope spectrin repeat protein 2) (Syne-2)
Nesprin 2 (Nuclear envelope spectrin repeat protein 2) (Syne-2)
Nesprin 2 (Nuclear envelope protein)
Nesprin 2 (Nuclear envelope protein)
Nuclear envelope protein)
SYNE2 OR NUA OR KIAA1011
SYNE2 OR NUA OR KIAA1011
SYNE2 OR NUA OR KIAA1011
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DOMAIN
                             SEQUENCE FROM N.A. (ISOFORMS 1 AND INTERACTION WITH F-ACTIN.
MEDLINB=22113112; PubMed=12118075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
CARBOHYD
                                                                                       Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; 3.
SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG_LIKE; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARSPLIC
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Alternative splicing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                          NKDGTYNWMSWLLVNTCAHRDDVVLTCQVEHDG-----QQAVSKSYALEI 348
                                                                                                                                                                                                                                                                                                                DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQL 628
                                                                                                                                                                                                                                                                                                                                                              AKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVL
                                                                                                                                                                                                                                                                                                                                                                                     QTNVDPAGDSVSYSIHSTARVVLTRGDVHSQVI-----CEMAHITLQGDPLRGTANLSE
                                                                                                                                                                                                                                                                                                                                                                                                            KTK--PREE----QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA-PIEKT--ISK
                                                                                                                                                                                                                                                                                                                                                                                                                                  PSAPVVSGPAV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH--EDPEVKFNWYVDGVEVHNA
                                                                                                                                                                                                                                                                                                                                       AIRVPPTLEV-TQQPMRAE----NQANVTCQVSNFYPRGLQLTWLENGNVSRTETASTLIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR007110; Ig-like.
IPR003597; Ig_c1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 147; DB
Pred. No. 0.02
41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
MISSING (in isoform 2
/FTId=VSP_007026.
R -> H (IN REF. 2; CA
D -> N (IN REF. 2; CA
M -> I (IN REF. 2; CA
M -> A (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IG-LIKE V-TYPE.
IG-LIKE C1-TYPE
IG-LIKE C1-TYPE
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                   ----RATPEHTVSFTCESHGFSPRDITLKWFKNGNELSDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL-REGULATORY PROTEIN BETA-1 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
                                                                                        Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
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H (IN REF. 2; CAC17540).

N (IN REF. 1).

I (IN REF. 2; CAB46661).

A (IN REF. 2).
                                                      9),
                                                      FUNCTION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                        Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.
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Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
Ak Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Ak Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Ak Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Ak Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Ak Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Ak Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Ak Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Ak Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Ak Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Ak Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Ak Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Ak Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Ak Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Ak Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Ak Villalon D.K., Wadan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Ak Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Ak Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Ak Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Ak Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Tomore T. M. A., Schein J.E., Jones S.J.M., Marra M.A.;
Tomore T. M. A., Schein J.E., Jones S.J.M., Marra M.A.;
Tomore T. M. A., Schein J.E., Jones S.J.M., Marra M.A.;
Tomore T. M. A., Schein J.E., Jones S.J.M., Marra M.A.;
Tomore T. M. A., Schein J.E., Jones S.J.M., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RA Heilig R., Eckenberg R., Petit J.-L., Fonknechten N., Da Silva C.,
RA Cattolico L., Levy M., Barbe V., De Berardinis V., Ureta-Vidal A.,
RA Pelletier E., Vico V., Anthouard V., Rowen L., Madan A., Qin S.,
RA Sun H., Du H., Pepin K., Artiguenave F., Robert C., Cruaud C.,
RA Bruels T., Jaillon O., Friedlander L., Samson G., Brottier P.,
RA Cure S., Segurens B., Aniere F., Samain S., Crespeau H., Abbasi N.,
RA Alach N., Boscus D., Dickhoff R., Dors M., Dubois I., Friedman C.,
RA Gouyvenoux M., James R., Madan A., Mairey-Estrada B., Mangenot S.,
RA Gouyvenoux M., James R., Madan A., Mairey-Estrada B., Mangenot S.,
RA Gouyvenoux M., James R., Madan A., Mairey-Estrada B., Mangenot S.,
RA Gouyvenoux M., James R., Madan A., Mairey-Estrada B., Mangenot S.,
RA Wacherie B., Bellemere C., Belser C., Besnard-Gonnet M.,
RA Vacherie B., Bellemere C., Belser C., Besnard-Gonnet M.,
Battol-Mavel D., Boutard M., Briez-Silla S., Combette S.,
RA Bartol-Mavel D., Boutard M., Briez-Silla S., Combette S.,
RA Magdelenat G., Pateau E., Petit E., Sirvain-Trukniewicz P., Trybou A.,
RA Wega-Czarny N., Bataille E., Bluet E., Bordelais I., Dubois M.,
RA Vega-Czarny N., Bataille E., Bluet E., Bordelais I., Dubois M.,
RA Dumont C., Guerin T., Haffray S., Hammadi R., Muanga J., Pellouin V.,
RA Abert D., Wunderle E., Gauguet G., Roy A., Sainte-Marthe L.,
RA Verdier J., Verdier-Discala C., Hillier L.W., Fulton L., McPherson J.,
RA Matsuda F., Wilson R., Scarpelli C., Gyapay G., Wincker P., Saurin W.,
"The DNA sequence and analysis of human chromosome 14.";
Nature 421:601-607(2003).
                  SEQUENCE
FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS 4; 5 AND 7).
SEQUENCE FROM N.A. (ISOFORMS 4; 5 AND 7).
MEDLINE-21652858; PubMed=11792814;
Zhang Q., Skepper J.N., Yang F., Davies J.D., Hegyi L.,
Weissberg P.L., Ellis J.A., Shanahan C.M.;
"Nesprins: a novel family of spectrin-repeat-containing
"Nesprins: a novel family of spectrin-repeat-containing
"Nesprins: a novel family of spectrin-repeat-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22388257;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Poustka A., Klein M.,
Submitted (SEP-1999)
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"The nesprins are giant actin-binding
Drosophila melanogaster muscle protein
Genomics 80:473-481(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=12508121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Testis;
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EMBL/GenBank/DDBJ databases
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                                                                                                                                                      human
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Newes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D., Wambutt R., Korn B., Klein M., Poustka A.;
"Towards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs.";
Genome Res. 11:422-435 (2001).

-i-FUNCTION: Involved in the maintenance of nuclear organization and structural integrity. Probable anchoring protein which theters the nucleus to the cytoskeleton. Connects nuclei to the cytoskeleton by interacting with the nuclear envelope and with F-actin in the Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O., Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H., Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Warakawa K., Kanehori K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B. Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Wiemann S., Weil B., Wellenreuther R., Gassenhube: Ansorge W., Boecher M., Bloecker H., Bauersachs S. Lauber J., Duesterhoeft A., Beyer A., Koehrer K., SEQUENCE OF 5754-6885 FROM N.A. MEDLINE=21154917; PubMed=11230166; Nakajima D., Okazaki N., Yamakawa H., K "Construction of expression-ready cDNA curation of 330 KIAA cDNA clones."; DNA Res. 9:99-106(2002). Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XII The complete sequences of 100 new cDNA clones from brain which code TISSUE-Brain TISSUE=Brain; MEDLINE=22158633; PubMed=12168954; MEDLINE=99246063; PubMed=10231032; SEQUENCE "NEDO human cytoplasm.

SUBCHLULAR LOCATION: Type IV membrane protein (Potential). The SUBCELLULAR LOCATION: Type IV membrane protein (Potential). The largest part of the protein is cytoplasmic, while its C-terminal part is associated with the nuclear envelope, most probably the outer nuclear membrane. Remains associated with the nuclear envelope during its breakdown in mitotic cells.

ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=9; large proteins in vitro."; Res. 6:63-70(1999). ime=4; Synonyms=Beta; IsoId=Q8WXH0-4; Sequence=VSP_007156. IsoId=Q8WXH0-7; Note=No experimental confirmation Note=Produced by Note=No IsoId=Q8WXH0-6; Sequence=VSP_007158, VSP
Note=No experimental confirmation availal IsoId=Q8WXH0-2; IsoId=Q8WXH0-1; Sequence=Displayed; ဝှု in cDNA sequencing project.";
(JUL-2002) to the EMBL/GenBank/DDBJ 5709-6885 experimental Sequence=VSP_007155; y exon skipping that nfirmation available; Sequence=VSP_007161, Sequence=VSP_007154, Sequence=VSP_007157, Sequence=VSP_007164, VSP FROM N.A. ence=VSP_007164, VSP_007166; confirmation available; (ISOFORM Kikuno R., Ohara O., Nagase T. A clones for KIAA genes: manual Gassenhuber J., Glassl auersachs S., Blum H., Koehrer K., Strack N., r B., Tampe J., Heubner 58, VSP 007165, available; 2) results VSP_007162 VSP_007163 VSP_007164, databases. ä ø VSP_007165; VSP_007166; S ₽ . ; ; ₩.

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Query Match
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Matches 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   targeting.
SIMILARITY: Belongs to the nesprin family.
SIMILARITY: Contains 1 actin-binding domain.
SIMILARITY: Contains 2 calponin-homology (CH) domair
SIMILARITY: Contains 1 Klarsicht domain.
SIMILARITY: Contains 13 leucine-rich (LRR) repeats.
SIMILARITY: Contains 9 spectrin repeats.
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IBOId=08WXH0-9; Sequence-VSp_007159, VSP_007160;
TISSUE SPECIFICITY: Widely expressed, with higher level in kidney, adult and fetal liver, stomach and placenta. Weakly expressed in skeletal muscle and brain. Isoform 5 is highly expressed in pancreas, skeletal muscle and heart.

DOMAIN: The Klarsicht domain mediates the nuclear envelope
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AF445011; AAL33548.1; -...
AY061757; AAL33801.1; -...
AY061759; AAL33801.1; -...
AY061759; AAL33802.1; -...
AF495911; AAN60443.1; -...
AL117404; CAB55905.1; -...
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AL355094;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 20.5
31; Conservative
EQKIERLLKCAS-----EIHMTLQPTAGGTSKNEGTITTSENRGGDPHSEAPFAKSDNQ
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                                         PAPIEKTISKAKGQPREPQVY-TLPPSRDELTKNQVSLTCLV-KGFYPSDIAVEWESNGQ
                                                                                          EKKLIRRGRTKGLIKEHEACFSEEGCLYQLNHHMEVLRELCEELPSQKSQQEVKRLLKDY
                                                                                                                                                                                     ----KMSLEEKSRDVCAKWESLHHE----LSLYVQQLKIDIEKGKLSDNILKLEKQINK
                                                                                                                                                                                                                                   PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK-----PREEQYNS
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Gene 55:75-84(1987).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
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                                                                                                                                                                                                                                          579
                                                                                                                                                                                                                                                                                                                                               521 QPR-EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP-ENNYKTTPPVLD 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  566
                                                                                                                                                                                        60
                                                                                                                                                                                                                                                                                                                                                                                                       34;
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Similarity 33.0%;
                                                                                                                                                                                        QNNKYMATSYLLLTAKAWETHSNYSCQVTHE---ENTVEKSLS
                                                                                                                                                                                                                                        SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
                                                                                                                                                                                                                                                                                               QPKATPSVTLFPPSSEELKTDKATLVCMVTDFYPGVMTVVWKADGTPITQGVETTQP-FK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NNKFRITSDFSSEEDRSSSCLQAKLTDLQVIKNETDARW 1170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17, Last sequence up 42, Last annotation
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17,
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                                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 146; DB 1;
Pred. No. 0.0047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERCHAIN (WITH HEAVY CHAIN)
; CBF71811F4BC878A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Deloukas P., Matthews L.H., Ashurst J., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Chagman J.C., Clamp M., Clark G.Y., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corrby N.R.,
RA Cligg S., Cobley V.E., Collier R.E., Connor R.E., Corrby N.R.,
RA Cligg S., Cobley V.E., Collier R.E., Connor R.E., Corrby N.R.,
RA Cligg S., Cobley V.E., Collier R.E., Connor R.E., Corrby N.R.,
RA Cligg S., Cobley V.E., Collier R.E., Connor R.E., Corrby N.R.,
RA Cligg S., Cobley V.E., Collier R.E., Connor R.E., Corrby N.R.,
RA Cligg S., Cobley V.E., Collier R.E., Connor R.E., Corrby N.R.,
RA Cligg S., Cobley V.E., Collier R.E., Connor R.E., Corrby N.R.,
RA Cligg S., Cobley V.E., Collier R.E., Connor R.E., Corrby N.R.,
RA Cligg S., Cobley V.E., Collier R.E., Connor R.E., Corrby N.R.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Milne S.A., Matry S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Matry S.L., Patel R., Pearce T.A.V., Peck A.I.,
RA Milne S.A., Matry S.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Wilmang L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Koepera J., Wasy P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
                RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Jordan B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Halton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Rahesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schewichenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schemitz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 414:865-871(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ichigotani Y., Matsuda S., Machida K., Oshi
Yamaki K., Hayakawa T., Hamaguchi M.;
"Molecular cloning of a novel human gene (S
member of the SIRP/SHPS-1 protein family.";
J. Hum. Genet. 45:378-382(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Lung;
MEDLINE=22388257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21638749;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
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     LOCATION:
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. 42, Last
/ protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=11780052;
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Primates;
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Catarrhini; Hominidae;
membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        precursor (SIRP-beta-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Χ.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SIRP-B2) which encodes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
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Query Match
Best Local (
Matches
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InterPro; IPR007110; Ig-like.
InterPro; IPR00597; Ig_Cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 3.
                                             CONFLICT
                                                                                                                                                                         TRANSMEM
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                     DOMAIN
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                             SMART; SM00407; IGcl; 2.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKB; 3.
PROSITE; PS00290; IG_MHC; FALSI
REPEAL; Signal; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -
                                     SEQUENCE
                                                                        VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement
                                                                                          VARSPLIC
                                                                                                  CARBOHYD
                                                                                                            CARBOHYD
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                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                        Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY:
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note=No experimental confirmation available; TISSUE SPECIFICITY: Detected in liver, and at very brain, heart, lung, pancreas, kidney, placenta and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTERNATIVE PRODUCTS:
Event=Alternative spl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=1
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BC020629;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note=No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q9P1W8-3;
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Similarity 57; Conserv
                                 286
387
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361
384
384
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146
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Conservative
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CAC00474.1;
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245
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317
33
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         4.3%;
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1 immunoglobulin-like V-type domain.
                                     MW:
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37;
                                                                                                N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
                                                                                                                                             CYTOPLASMIC (POTI
IG-LIKE V-TYPE.
IG-LIKE C1-TYPE:
IG-LIKE C1-TYPE:
POTENTIAL.
POTENTIAL.
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A -> V (IN REF. 2)
L -> S (IN REF. 2)
         Pred.
                  Score
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                                     F7F20C9F86E0E64B
Mismatches
       ≥ 146; -
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          .027;
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                  Length 387;
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Indels
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22;
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Gaps
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ELIGGPSV-FLFPPKPKDTLMIS----RTPEVTCVVVDVSH--EDPEVKFNWYVDGVEVH 464

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RESULT 93
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DISULFID
VARIANT
SEQUENCE
                                                                                                                                                                                                                                                         Pfam; PF00047; 19; 1.
SMART; SM00407; IGC.; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C
                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation updat
19 lambda chain C region.
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-87218480; PubMed-3107981; Parvari R., Ziv E., Lentner F., Tel-Or S., Burstein Y., Schechter I.; "Analyses of chicken immunoglobulin light chain cDNA clones indicate a few germline V lambda genes and allotypes of the C lambda locus."; EMBO J. 6:97-102(1987).
                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X04768; CAA28461.1; -. PIR; B26167; B26167.
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01-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                 NON_TER
                                                                                                                                                                                                                                                                                                                                    InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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                                                                                   521 QPR-EPQVYTLPPSRDELTK-NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 578
60
                                                                                                                                 Similarity
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SNSQYMASSYLSLSASDWSSHETYTCRVTH
                          SDGSFFLYSKLTVDKSRWQQGNVFSCSVMH
                                                       QPKVAPTITLFPPSKEELNEATKATLVCLINDFYPSPVTVDWVIDGSTRSG-ETTAPQRQ
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BARAR

C166 CARAU Q90304; 01-NOV-1997 30-MAY-2000 10-OCT-2003

(Rel. (Rel.

35, 39,

Created)
Last sequence update)
Last annotation update)

STANDARD;

555

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RESULT 95
C166_CARAU
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KACB_RAT
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Matches 29
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DISULFID 26

CONFLICT 30

CONFLICT 48

CONFLICT 8:

CONFLICT 8:

CONFLICT 9:

CONFLICT 9:

CONFLICT 10:
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Rattus norvegicus (Rat).
Eukarvota: Martin (Rat).
                                                                                                                                                                                                                                                                                                                            Pfam; PF00047; ig; 1.

SMART; SM00407; IGcl; 1.

PROSITE; PS0835; IG_LIKE; 1.

PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sheppard H.W., Gutman G.A.; "Allelic forms of rat kappa chain genes: evidence selection at the level of nucleotide sequence.";
                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                             selection at the level Proc. Natl. Acad. Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seq
10-OCT-2003 (Rel. 42, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P01842; 2MCG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Starace V., Querinjean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE (BENCE-JONES PROTEIN S211).
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=75212238; PubMed=807630;
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                                              60
                                                                                        ຫ
                                                                                                                                    l Similarity
29; Conserv
                                              SKDSTYSMSSTLSLTKADYESHNLYTCEVVHK 91
                                                                                                       PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS-----
                                                                  -- DGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 609
                                                                                        PTVSIFPPSTEQLATGGASVVCLMNNFYPRDISVKWKIDGTERRD-----GVLDSVTDQD 59
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106
20
30
48
79
87
98
                                                                                                                                  4.2%;
llarity 31.5%;
Conservative 2
                                                                                                                                                                                                                                                                                                                   domain; Immunoglobulin
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                                                                                                                                                                                11601 MW; 4CFA7CA820D1CA36 CRC64;
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                                                                                                                                     22;
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D - N (IN REF. 2).

N - N (IN REF. 2).

MISSING (IN REF. 2).

E -> Q (IN REF. 2).

E -> Q (IN REF. 2).

V -> VW (IN REF. 2).

V -> VW (IN REF. 2).
                                                                                                                                  Score 145; DB 1;
Pred. No. 0.0056;
2; Mismatches 2
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PROSITE; PS00290; IG_MHC; 1.

Signal; Developmental protein; Cell adhesion; Immunoglobulin

Repeat; Glycoprotein; Transmembrane.
                                                                                                                                                                                                                                                                                  Pfam; PF00047; ig; 3.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                     InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                         PIR; I50478; I50478.
HSSP; Q13740; 1KJC.
                                                                                                                                                                                                                                                                                                                                                                EMBL; L25056; AAC38015.2; -.
                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Differentiation 56:21-29(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laessing U., Giordano S., Stecher B., Lottspeich F., Stuermer C.A. "Molecular characterization of fish neurolin: a growth-associated cell surface protein and member of the immunoglobulin superfamily the fish retinotectal system with similarities to chick protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD166 antigen homolog precursor (Neurolin) Carassius auratus (Goldfish).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: CELL ADHESION MOLECULE. INVOLVED IN NEURITE EXTENSION E REURONS VIA HETEROPHILIC AND HOMOPHILIC INTERACTIONS.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: PRESENT ON ALL RETINAL GANGLION CELLS (RGCS)
AND THEIR AXONS (IN EMBRYO). ABSENT FROM MATURE AXONS ALONG MOST OF THEIR LENGTH, BUT IS PRESENT ON UNW AND GROWING AXONS DERIVED FROM THE RGCS AT THE RETINAL MARGIN. REMAINS ON ADULT RGCS ONLY A CELL-CELL CONTACT SITES AND IS CONTINUOUSLY FOUND IN THE RETINAL AXON TERMINAL ARBOR LAYERS OF THE ADULT TECTUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Contains 3 immunoglobulin-like C2-type domains SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                    European
                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a case the Swiss Institute of Bioinformatics and the EMBL
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Carassius.
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                                                                                                  IG-LIKE V-TYPE 1.
IG-LIKE V-TYPE 2.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
POTENTIAL.
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CYTOPLASMIC (POTENTIAL).
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Ostariophysi; Cypriniformes;
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                                           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-92031698; PubMed=1932117;
MCDayashi M., Miura M., Asou H., Uyemura
Kobayashi M., Miura M., Asou H., Uyemura
"Molecular cloning of cell adhesion molecular cloning of the primary sequence."
                                                                                                                                                                              p32004; Q8TA87;
01-JUL-1993 (Rel. 24, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Neural cell adhesion molecule L1 precursor (N-CAM
L1CAM OR CAML1 OR MIC5.
                                       tissue: a comparison of the different origin.";
                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                           Biochim.
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hes 119; Conserv
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; Primates;
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Pred. No. 0.053;
9; Mismatches 209;
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SEQUENCE

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MEDIINE-2338257; PubMed=12477932;

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Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                     Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                           molecule
J. Biol.
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"A human brain
                                                                                                                                                                                                                                                                                                                       Djabali M., Mattei M.-G., Nguyen C., Roux D., Demengeot J., Denizot F., Moos M., Schachner M., Goridis C., Jordan B.R., "The gene encoding L1, a neural adhesion molecule of the immunoglobulin family, is located on the X chromosome in mor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomics
                                                                                                                                                                             Nucleic Acids
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Rosenthal A., Mackinnon R.N., Jones D.S.C.;
"PCR walking from microdissection clone M54
from the human gene for the neural cell adh
                                                                                                                                                                                                                                                         SEQUENCE OF 353-117
TISSUE=Fetal brain;
                                                                                                                                                                                         from the human (CAM-L1).";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND ALTERNAT MEDLINE-98147998; PubMed-9479034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=88298876;
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MEDLINE-92120663; PubMed=1769655;
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"Molecular structure and functional
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R., Mujoo K., S
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EMBL/GenBank/DDBJ
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Kenwrick S.,
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MEDLINE=98180721; PubMed=9521.424;
DU Y.-Z., Srivastava A.K., Schwartz C.E.;
"Multiple exon screening using restriction endonuclease fingerprinting (REF): detection of six novel mutations adhesion molecule (L1CAM) gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97338664; PubMed=9195224;
Macfarlane J.R., Du J.-S., Pepys M.E., Ramsden S., Donna Charlton R., Garrett C., Tolmie J., Yates J.R.W., Berry Moncla A., Lunt P., Hodgson S., Jouet M., Kenwrick S.; "Nine novel L1 CAM mutations in families with X-linked hydrocephalus.";
Hum. Mutat. 9:512-518(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [19]
VARIANTS HSAS/MASA/SPG1 SER-179 AND ARG-370.
MEDLINE=96057511; PubMed=7562969;
Puris J. C.. Cuppens H., Legius E., Fryns J.-P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Engel W., Schwinger E., Gal A.; "Five novel mutations in the LICAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97083370; F
Gu S.-M., Orth U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Mutations in L1-CAM in two families with X linked complicated spastic paraplegia, MASA syndrome, and HSAS."; J. Med. Genet. 32:549-552(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruiz J.C., Cuppens Cassiman J.-J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANTS HSAS GLN-184;
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                            LMISRTPEVTCVVVDVSHED-----PEVKFNWYVDGVEVHN------AKTKPR
                                                        QIVSD--PFLVVSNTSTFVPYEIKVQAVNSQGK--
                                                                                  CLLSDSGQVLLESNIKVLPTWSTPVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT
                                                                                                                                       MRATQLQKNLTCEVWGP-----TSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQ-
                                                                                                                                                                      FRVTAINKYGPGEPSPVSETVVTPEAAPEKNPVDVKGEGNET
                                                                                                                                                                                               KRYTQDPKLQMGKKLPLHLTL--PQALPQ-----YAGSGNLTLALEAKTGKLHQEVNLVV
                                                                                                                                                                                                                            TOSOVRVSWSPAEDHNAPIEKYDIEFEDKEMAPEKWYSLGKVPGNOTSTTLKLSPYVHYT
                                                                                                                                                                                                                                                        EGEQVEFSFPLA-----FTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSV
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 ·PQVT---IGYSGEDYPQAIPE-----LEGIEILNSSAVLVKWRPVDLAQVKGH
                                                                                                              -----TWKPLRWMDWNAPQVQYRVQ
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r E., Gal A.;
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Pfam; PF00047; ig; 6.
SMART; SM00060; FN3; 2.
SMART; SM00408; IGc2; 5.
PROSITE; PS50835; IG_LIKE; 6.
Neurogenesis; Cell adhesion; De
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01-OCT-1989
15-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Neural adhesion molecule L1 as a member superfamily with binding domains similar Nature 334:701-703(1988).
                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAML_MOI
P11627;
              CHAIN
DOMAIN
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Mammalia; Eutheria; Rodentia;
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Mus musculus (Mouse)
                                            SIGNAL
                                                                                                                                                                                                                 MGD; MGI:96721; Llcam.
GO; GO:0007411; P:axon guidance; IMP
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                                                                                                                                                                                                                                                                                                                     entities requires a license agreement
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                                                                                                                                                                    InterPro; IPR008957; FN_III-like.
InterPro; IPR003961; FN_III.
InterPro; IPR007110; Ig-like.
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 TRANSMEM
                                                        Neurogenesis; Cell adhesion; Developmental protein;
Transmembrane; Repeat; Immunoglobulin domain; Signa
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SIMILARITY: Belongs to the immunoglobulin superfamily.
Ll/neurofascin/NgCAM family.
SIMILARITY: Contains 6 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 5 fibronectin type III domains.
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(Rel. 12, Last sequence update)
(Rel. 43, Last annotation update)
adhesion molecule L1 precursor (N-CAM
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 EXTRACELLULAR POTENTIAL.
                            NEURAL CELL ADHESION MOLECULE L1
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                              VSKREKPVWVLNPEAGMWQCLLSDSGQV---LLESNIKVLPTWSTPVEPKSCDKTHTCPP
                                                                                                                                                                   SWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLH
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19.9%;
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IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 4.

IG-LIKE C2-TYPE 5.

IG-LIKE C2-TYPE 5.

IG-LIKE C2-TYPE 5.

IG-LIKE C2-TYPE 6.

FIBRONECTIN TYPE-III 1.

FIBRONECTIN TYPE-III 2.

FIBRONECTIN TYPE-III 3.

CCELL ATTACHMENT SITE (POTE BY SIMILARITY.

BY SIMILA
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MOUSE
KAC_
"Expression in non-lymphoid cells of mouse recombinant directed against the tumour marker human placement phosphatase.";
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21-JUL-1986
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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10-OCT-2003 (Rel. 42, Lag
Ig kappa chain C region.
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Altenburger W., Neumaier P.S., Steinmetz M.,
"DNA sequence of the constant gene region of
                                                                                                                                                                                                                                                                                                       Max E.E., Maizel J.V. Jr., Leder P.;
"The nucleotide sequence of a 5.5-kilobase DNA segment containing mouse kappa immunoglobulin J and C region genes.";
J. Biol. Chem. 256:5116-5120(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE=82059477; PubMed=6170937;

Hamlyn P.H., Gait M.J., Milstein C.;

Hamlyn P.H., Gait M.J., Milstein Ci;

"Complete sequence of an immunoglobulin mRNA using and the dideoxynucleotide method of RNA sequencing. Nucleic Acids Res. 9:4485-4494(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequencing.";
Cell 15:1067-1075(1978).
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MEDLINE=73053310; PubMed=4638343;
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plete amino acid sequence
J. 128:427-444(1972).
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MOUSE STANDARD; PRT; 837 AA.

035136; 035962;

15-JUL-1998 (Rel. 36, Created)

15-JUL-1998 (Rel. 36, Last sequence update)

10-OCT-2003 (Rel. 42, Last annotation update)

Neural cell adhesion molecule 2 precursor (N-CAM
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SMART; SM00407; IGcl; 1.
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MGD;
                                                                                               STRAIN=BALB/c; TISSUE=Olfactory neuroepithelium; MEDLINE=97368238; PubMed=9221781; Yoshihara Y., Kawasaki M., Tamada A., Fujita H., Kagamiyama H., Mori K.; "OCAM: A new member of the neural cell adhesion"
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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NCAM2 OR OCAM OR RNCAM.
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SIMILARITY: Contains 1 immunoglobulin-like domain.
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Pred. No. 0.0075;
8; Mismatches 33;
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DR InterPro; IPR008957; PN II
DR InterPro; IPR008957; FN II
DR InterPro; IPR003961; FN II
DR InterPro; IPR003961; FN II
DR InterPro; IPR007110; Ig-11k
DR InterPro; IPR007110; Ig-2-11k
DR InterPro; IPR003598; Ig-2-2
NR Pfam; PF00041; fn3; 2.
R Pfam; PF00047; ig; 5.
R SMART; SM00060; FN3; 2.
R SMART; SM00060; FN3; 2.
R PR0SITE; PS50835; IG_LIKE; 5.
Cell adhesion; Transmembran-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [2]
SEQUENCE FROM N.A. (ISOFORM SHORT).
STRAIN=C57BL/6J; TISSUE=Olfactory epithelium;
MEDLINE=97476194; PubMed=9334170;
Alenius M., Bohm S.;
                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: May play important roles in selective fasciculation zone-to-zone projection of the primary olfactory axons.
-!- SUBCELIULAR LOCATION: Type I membrane protein (long isoform)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Identification of a novel neural cell adhesion molecule-related with a potential role in selective axonal projection.";
J. Biol. Chem. 272:26083-26086(1997).
                                                                                CARBOHYD
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                                           CARBOHYD
                                                              CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      attached to the membrane by a GPI-anchor (short isoform).
ALTERNATIVE PRODUCTS:
Event_Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=Short;
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AF001286;
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                      ; FN_III-like.
; FN_III.
; Ig-like.
; Ig_c2.
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N-LINKED (GLCNAC...) (POTENTIAL).
TLYNCLGLGALIGLGYAALLLILVYDYSCFFIROCGILMC
ITRRNCGKKSGSSGKSKELEEGKAAYLKDGSKEPIVEMRTE
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IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
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                                                                                                                                                                                                                                                                                                      TYPE-III
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Matches 101
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                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
Barton C.H., Dickson G., Gower H.J., Rowett L.H., Putt W., Elsom V., Moore S.E., Goridis C., Walsh F.S.; "Complete sequence and in vitro expression of a tissue-specific phosphatidylinositol-linked N-CAM isoform from skeletal muscle.";
                                                            SEQUENCE FROM N.A. (ISOFORM N-CAM 120).
TISSUE=Skeletal muscle;
MEDLINE=89305258; PubMed=3253057;
                                                                                                                                                                                     NCAM1 OR NCAM
                                                                                                                      NCBI_TaxID=9606;
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Pred. No. 0.13;
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ETIEIKVSNDIIQSKEDDIKA -> NCCEANKGENGGOSWH
LNAVGETFVITMSLSCLF (in isoform Short).
/FTId=VSP_002590.
                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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GO; GO:0005886; C:plasma membrane; TAS.
InterPro; IPR008957; FN_III-like.
InterPro; IPR003961; FN_III.
InterPro; IPR003961; FN_III.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
Pfam; PF00041; fi3; 2.
Pfam; PF00047; ig; 5.
SMART; SM00408; FN3; 2.
SMART; SM00408; IGc2; 5.
SMART; SM00408; IGc2; 5.
PROSITE; PS50835; IG LIKE; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X16841; CAA34739.1; -. EMBL; M17409; AAA59912.1; -. EMBL; M22094; AAA59910.1; -. EMBL; M22092; AAA59911.1; -- EMBL; M22091; AAA59911.1; JOIN PIR; A31635; A31635.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-87301755; PubMed=2887295;
Dickson G., Gower H.J., Barton C.H., Prentice H.M., Elsom V., Moore S.E., Cox R.D., Quinn C., Putt W., Walsh F.S.;
"Human muscle neural cell adhesion molecule (N-CAM): identif of a muscle-specific sequence in the extracellular domain.";
Cell 50:1119-1130(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 491-69 MEDLINE=89077552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 491-761 FRO
TISSUE=Skeletal muscle;
                                                                                                                                                                 GPI-anchor; Alternative
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PIR; S07784; IJHUNG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Attached to the membrane ALTERNATIVE PRODUCTS: Event-Alternative splicing; Named isoforms=3; Name=N-CAM 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=N-CAM 140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=P13592-2; Sequence=Displayed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               non-profit institutions as long and this statement is not removed. requires a license agreement (See an email to license@isb-sib.ch).
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          3, 2004, 13:09:00
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Result
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Maximum Match 100%
Listing first 125 summaries
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InterPro; IPR000973; CD4 TCAg.
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Pfam; PF00047; ig; 2.
PRINTS; PR00692; CD4TCANTIGEN.
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O1-JUL-1997 (TrEMBLrel. 0
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CD4 (Fragment).
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Fonsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., M. Corbet S., Barre-Sinoussi F., Allan J.S.;
"Relation between phylogeny of African green monkey CD4 their respective simian immunodeficiency virus genes.";
J. Med. Prinatol. 26:120-128(1997).
EMBL; AP001225; AAB60872.1; -.
HSSP; P01730; 1WIQ.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0016955; P:immune response; IEA.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
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O7z120 caenorhabdi
Q96e61 homo sapien
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Q8mns0 caenorhabdi
Q8mns1 caenorhabdi
Q8mns1 caenorhabdi
Q8isf6 caenorhabdi
Q8isf7 caenorhabdi
Q8isf7 caenorhabdi
Q99m11 mus musculu
Q90ym2 brachydanio
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Q96as2 homo sapien
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Q96i69 homo sapien
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InterPro; IPR003596; Ig_v.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                      MEDLINE=98017879; PubMed=9379478; Fomsgaard A., Muller-Trutwin M.C.
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Pred. No. 3.6e-
16; Mismatches
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Best Local S
Matches 330
                                                                                                                                                                                                             Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J.,
Corbet S., Barre-Sinoussi F., Allan J.S.;
"Relation between phylogeny of African green monkey CD4
their respective simian immunodeficiency virus genes.",
J. Med. Primatol. 26:120-128(1997).
EMBL; APRO1227; ABB60974.1; -
GO; GO:0016020; C:membrane; IEA.
GO; GO:006955; P:immune response; IEA.
InterPro; IPR000973; CD4 TCAG.
InterPro; IPR001710; Ig-Tike.
InterPro; IPR001710; Ig-Tike.
InterPro; IPR001710; Ig-Tike.
InterPro; IPR001710; Ig-Tike.
Query Match
Best Local Similarity
                                                                                      Pfam; PF00047; 1g; 2.
PRINTS; PR00692; CD4TCANTIGEN.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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                                                                   SEQUENCE
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Pred. No. 7.3e-122;
.7; Mismatches 22;
Score
Pred.
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Catarrhini;
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                                                                 21C3E30882ABFBC0 CRC64;
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1709; DB 6;
No. 8.7e-122;
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Query Match
Best Local Similarity
Matches 329; Conserv
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Fonmsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., M. Corbet S., Barre-Sinoussi F., Allan J.S.;
"Relation between phylogeny of African green monkey CD4 their respective simian immunodeficiency virus genes.";
J. Med. Primatol. 26:120-128(1997).
EMBL; AF001123; AAB60870.1; -.
HSSP, P01730; 1WIO.
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Pfam; PF00047; ig; 2.
Ponn692; CD4TCANTIGEN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithe
Cercopithecinae; Cercopithecus.
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SMART; SM00406; IGV; 1.
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GO; GO:0006955; P:limune response;
InterPro; IPR000973; CD4 TCAg.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                 PROSITE; PS50835; IG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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397 AA;
Conservative
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Score 1705; DB 6;
Pred. No. 1.8e-121;
.8; Mismatches 22;
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                                                                                             7CE39AD0F8506C81 CRC64;
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                                                                                              Query Match
Best Local Similarity
Matches 329; Conser
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GO; GO:0006955; P:immune response; II
InterPro; IPR00973; CD4 TCA9.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 2.
PRINTS; PR00692; CD4TCANTIGEN.
SWART; SM00406; IGv; 1.
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O09263;
O1-JUL-1997 (TrEMBLrel. 0
O1-JUL-1997 (TrEMBLrel. 0
O1-OCT-2003 (TrEMBLrel. 2
CD4 (Fragment).
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF001222; AAB60869.1; -. HSSP; P01730; 1WIQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Cercopithecinae; Cercopithecinae;
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VVLGKKGDTVELTCNASQNTTTQFHWKNSNQIKILGKQGSFLTKGSSKLRDRIDSRKSLW
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Pred. No. 1.8e-1;
16; Mismatches (
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MEDLINE-98017879; PubMed-9379478;

FORMSGAARD A., Muller-Trutwin M.C., Diop O., H
FORMSGAARD A., Sarre-Sinoussi F., Allan J.S.;

"Relation between phylogeny of African green
their respective simian immunodeficiency viru
J. Med. Primatol. 26:120-128(1997).
                                                                                                                                                                                    GO; GO:0016020; C:membrane; IEA.
GO; GO:0006955; P:immune response;
InterPro; IPR000973; CD4 TCA9.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 2.
                                                                                                                                                                                                                                                                                                                                                       Cercopithecinae;
NCBI_TaxID=60712;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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DOGCESMIIKNLKIEDSETYICEVENKKEEVELLVEGLTANSDTHLLOGOSLTLTLESPP
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C -!- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).

C -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

C -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

C -!- SUMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS

C -!- SUMILARITY: BLONGS TO THE LAMUNOGLOBULIN SUPERFAMILY. CONTAINS

C -!- SUMILARITY: BELONGS TO THE LAMUNOGLOBULIN SUPERFAMILY. CONTAINS

C -!- SUMILARITY: BUDNALINS.

DR EMBL; AF001226; AAB60873.1; -.

DR EMBL; AF001226; AAB60873.1; -.

DR EMBL; AF0012380; AAC25124.1; -.

DR HSSP; P01730; IMIQ.

DR HSSP; P01730; IMIQ.

DR GO: G0:0016951; P:immune response; IEA.

DR GO; G0:0016951; P:immune response; IEA.

DR InterPro; IPR000973; CD4 TCA9.

DR InterPro; IPR00396; IG4 TCA9.

DR PAINTS; PR00692; CD4TANTIGEN.

DR SMART; SM00406; IGV; 1.

KW Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;

KW Lipoprotein; Palmitate; Repeat.
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O02805; O77593;

01-JUL-1997 (TrEMBLrel. 04, C:
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T-cell sufface glycoprotein C
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Harris E.E., Disotell T.R.;
"Nuclear gene trees and the phylogenetic relationships of the mangabeys (primates: Papionini).";
Mol. Biol. Evol. 15:892-900(1998).
-I-FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Peripheral blood;
MEDLINE=98017879; PubMed=9379478;
Pomsgaard A., Mueller-Trutwin M.C., Diop O., Hansen Corbet S., Barre-Sinoussi F., Allan J.S.;
"Relation between phylogeny of African green monkey their respective seintan immunodeficiency virus genes J., Med. Primatol. 26:120-128(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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NCBI_TaxID=9534;
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                                                                                                                                                                                                 Score 1697; DB 6;
Pred. No. 7.2e-121
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MEDLINE=22174698; PubMed=12186836;
LaBonte J.A., Babcock G.J., Patel T., Sodros,
"Blockade of HIV-I Infection of New World Mo
Primarily at the Stage of Virus Entry.";
J. Exp. Med. 196.431-445(2002).
EMBL; AF452617; AAN14533.1; -.
GO: GO:001620; C:membrane; IEA.
GO: GO:0006955; P:immune response; IEA.
GO: GO:0006955; P:immune response; IFA.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 2.
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GO; GO:0006955; P:immune response; IE
InterPro; IPR00393; CJ_TCAG.
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InterPro; IPR003599; Ig_V.
InterPro; IPR003596; Ig_V.
IfterPro; IPR003596; Ig_V.
PFAM; PF00047; Ig; 2.
PRINTS; PR00692; CD4TCANTIGEN.
SMART; SM00406; IG; 3.
SMART; SM00406; IG; 3.
SMART; SM00406; IG; 1.
PROSITE; PS50835; IG_LIKE; 1.
SEQUENCE 457 AA; 50878 MW; 718CFE
                                                                                                                                                                                                                                                                                                                                                          Ol-OCI-2000...
Lymphocyte antigen CD4.
Salmiri Bciureus (Common squirrel monkey).
Salmiri Bciureus (Common Squirrel monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordates; Platyrrhini; Cebidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QBHZT7; PRELIMINARY;
QBHZT7; PRELIMINARY;
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
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Cebinae; Saim
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               RC TISUE-Spieen;

RX MEDIJINE-22388557, bubMed=12477932;

RX MEDIJINE-22388557, bubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hosh J.,

RA Hopkins R.F., Jordan H., Moore T., Max R., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Moltinge A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Geners I.O., Dickson M.C.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Geners I.O., Dickson M.C.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Geners I.O., Dickson M.C.,

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Best Local S
Matches 310
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Homo sapiens (Human).
Bukaryota; Metazoa; Ch.
Mammalia; Eutheria; Pr.
NCBI TaxID=9606;
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Q7Z5W1;
Q7Z5W1;
Q7Z5W1;
Q1-OCT-2003 (TrEMBLrel.:
Q1-OCT-2003 (TrEMBLrel.:
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SMART; SM00409; IG; 3.
SMART; SM00406; IGy; 1.
PROSITE; PS50835; IG LIKE;
SEQUENCE 457 AA; 50899 N
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   'Generation
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   and
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Primates;
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%; Pred. No. 3.2e
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Last sequence update)
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RESULT 11
Q727P5
ID Q727P
AC Q727P
AC Q727P
DT 01-00
DT 01-00
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DT Hypot
OS Homo
OC Eukaz
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RN [1]
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Best Local S
Matches 292
Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; C:
Mammalia; Eutheria; Primates; C:
NCBI TaxID=9606;
[1]
                                                                           Q7Z7P5
Q7Z7P5;
Q1-OCT-2003
01-OCT-2003
01-OCT-2003
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Submitred (JUN-2003) to the EM
EMBL; BC053984; AAH53984.1; -.
Hypothetical protein.
SEQUENCE 470 AA; 51204 MW;
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TISSUE Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.
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                                                                                                                                                                                                                                                                                                                                                                                                           LLESNIKVLPTWSTPVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV
---SNTKV----DKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV
                                                                                                                                                                                                                          SLSLSPG
                                                                                                                                                                                                                                                                 EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK
                                                                                                                                                                                                                                                                                                                   KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
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                                                                                                                                                                                                SLSLSPG
                                                                                                                                                                                                                                                  EWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK
                                                                                                                                                                                                                                                                                                      KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
                                                                                                                                                                                                                                                                                                                                                          TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
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                                                                           (TrEMBLrel.
(TrEMBLrel.
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, Last annotation v
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Pred. No. 8.
                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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QBNFI I2
QBNFI ID QBNFI ID QBNFI ID QBNFI ID O1-OC DT 01-OC DT FLJOO GN FLJOO GN FLJOO OS Homo OC Euchama OX NCBI RN [1]

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Best Local S
Matches 236
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., Wcrley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Alnes S. I. Malska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Alnes S. I. Malska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                     Q8NF17;
                                                                                                                           01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2003 (TrEMBLrel. 25,
FLJ00385 protein (Fragment)
FLJ00385,
SEQUENCE FROM N.A. TISSUE=Spleen;
                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
TISSUE=Spleen;
                                                  NCBI_TaxID=9606;
                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical SEQUENCE 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-2003) to the EMBL/GenBank/DDBJ EMBL; BC051328; AAH51328.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                     LSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNIKVLPTWSTPVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK
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                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                     Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51395 MW;
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Last sequence update)
Last annotation updat
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Pred. No. 6.1e-88;
0; Mismatches 4
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Best Local Similarity
Matches 235; Conserv
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Q7Z351;
Q7Z351;
Q7Z351;
Q7Z351;
Q7Z351;
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Q1-QCT-2003 (TrEMBLrel. 25, Last sequence update)
Q1-QCT-2003 (TrEMBLrel. 25, Last annotation update)
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PIR; A45874; A45874.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 3.
SWART; SW00407; IGc1; 3.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PROSITE; NON TER SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

TISSUB-Human rectum tumor;

Bloecker H., Boccher M., Mewes H.W., Weil B., Amid C., C
Bloecker H., Buccher M., Mewes H.W., Weil B., Amid C., C
Fobo G., Han M., Wiemann S.;

Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BX538118; CAD98026.1; -.
                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein. SEQUENCE 482 AA; 52852 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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; Pred. No. 8.1e-88;
11; Mismatches 10;
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                                                                                                                                                                                                                 Score 1264.5; DB 4; Pred. No. 8.2e-88; 0; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     089498D8076E863C CRC64;
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GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IE
InterPro; IPR000152; Asx hydroxyl S.
InterPro; IPR000152; Asx hydroxyl S.
InterPro; IPR000142; EGF 2.
InterPro; IPR00142; EGF 2.
InterPro; IPR001438; EGF II.
InterPro; IPR001438; EGF II.
InterPro; IPR001438; EGF II.
InterPro; IPR00239; EGF like.
InterPro; IPR00230; EGF like.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003597; Ig_C1.
InterPro; IPR00314; Peptidase S1.
InterPro; IPR001314; Peptidase S1.
InterPro; IPR001314; Peptidase S1.
InterPro; IPR001314; Peptidase S1.
InterPro; IPR001314; Peptidase S1.
Pfam; PF00008; EGF; 2.

Pfam; PF000047; ig; 2.

Pfam; PF00047; ig; 2.

Pfam; PF00047; ig; 2.

Pfam; PF00049; trypsin; 1.

PFINTS; PR00010; EGFBLCOD.

PRINTS; PR00010; GLBLCOD.

PRINTS; PR00011; EGF; 2.

SMART; SM00181; EGF; 2.

SMART; SM00179; EGF CA; 1.

SMART; SM00069; GLA; 1.

SMART; SM000007; IGC1; 2.

SMART; SM000007; IGC1; 2.

SMART; SM0000007; IGC1; 2.

SMART; SM00000007; IGC1; 1.

PROSITE; PS0000022; EGF_1; 1.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Factor VII active site mutant immunoconjugate.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hu Z., Garen A.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ
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Hu Z., Garen A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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Best Local S
Matches 231
                                                   Query Match
Best Local S
Matches 254
                                                                                                 MEDINE-19716435; PubMed-10199913;
Romano T.A., Ridgway S.H., Felten D.L., Qua "Molecular cloning and characterization of the white whate Deliphinapterus leucas.";
Immunogenetics 49:376-383(1999).
EMBL; AP071799; AAD23738.1; -.
HSSP; P01730; IWIQ.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0006925; P:immune response; IEA.
InterPro; IPR000973; CD4 TCAg.
InterPro; IPR00310; Ig_Tike.
InterPro; IPR003596; Ig_V.
PEam; PF00047; 1g; 3.
PRINTS; PR00692; CD4TCANTIGEN.
SMART; SM00406; IGV; 1.
SMART; SM00406; IGV; 1.
SEQUENCE 455 AA; 50499 MW; AA532FD4411A
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Q9XS78;
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01-NOV-1999 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
T-cell surface glycoprotein CD4.
Tell surface glycoprotein CD4.
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9749;
                                                                                                                                                                                                                                                                                                                                                                             Monodontidae; Delphinapterus.
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2; PS001187; EGF_CA; 1.
3; PS00011; GLU_CARBOXYLATION; 1.
3; PS50835; IG_LIKE; 2.
2; PS000290; IG_MHC; 1.
3; PS50240; TRYPSIN_DOM; 1.
3; PS000134; TRYPSIN_HIS; 1.
3; PS00135; TRYPSIN_SER; 1.
3; PS00135; TRYPSIN_SER; 1.
3; PS00135; TRYPSIN_SER; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
            MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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MDPRTSLRHLFLVLQLVMLPAGTQGKKVVLGKAGELAELPCKASQNKSLFFSWKNSYQTK
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                                                  Score 1185.5; DB 6
Pred. No. 7.8e-82;
6; Mismatches 107;
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Pred. No. 4.2e-87;
0; Mismatches 0;
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S; 1.
R; 1.
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                                                                                  Query Match
Best Local S
Matches 214
                                                                                                                                                                                                                                                                                                       ITISSUE=Placenta;
Li W.B., Gruber C., Jessee J., Polayes D.;
"Full-length cDNA libraries and normalization.";
Submitted (FEB-2003) to the EMBL/GenBank/DD5J datab
EMBL; BX248278; CAD62606.1; -.

R GO; GO:0046827; C:extrachromosomal DNA; IEA.
R InterPro; IPR007110; Ig-like.
R InterPro; IPR003597; Ig_cl.
R InterPro; IPR003066; Ig_MHC.
                                                                                                                                                                                                           Interero; IPRUUJU.
Interero; IPRUUJU.
Interero; IPRUUJU.
Pfam; PF00047; ig; 1.
SMART; SM00407; IGc1; 3.
SMOART; PS50835; IG LIKE; 3.
TOASITE; PS50835; IG_MHC; 2.
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Q86TT2;
01-JUN-2003 (TrEMBLrel. 24, Cro
01-JUN-2003 (TrEMBLrel. 24, Las
01-OCT-2003 (TrEMBLrel. 25, Las
Human full_length cDNA clone C
                                                                                                                                                                                            Plasmid.
                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Placenta;
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                                                                                  Local Sim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Human)
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                                                                                                       Similarity
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BPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NL--TKGKLYQEVNLVVMRVTKSPNSLTCEVLGPTSPRLILSLKKENQSMRVSDQQKLVT
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                                                                                                                                                                        354 AA;
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                                                                                     Conservative
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Last annotation updat
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                                                                                  Score 1171; DB Pred. No. 7e-81; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                          23B80BF4D2B87A92
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RESULT 18
Q8TC63
ID Q8TC6
AC Q8TC6
AC Q8TC6
DT 01-JU
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Best Local
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InterPro; IPR007110; Ig-like.

InterPro; IPR003597; Ig_cl.

InterPro; IPR003596; Ig_MHC.

InterPro; IPR003596; Ig_v.

Pfam; PP00047; Ig' 4.

SWART; SW00407; IG'; 3.

SMART; SW00406; IGv; 1.

PROSITE; PS00835; IG LIKE; 4.

PROSITE; PS00835; IG MHC; 2.

Hypothetical protein.

SEQUENCE 521 AA; 57156 MW;
Q8TC63;
Q8TC63;
01-JUN-2002
01-JUN-2002
01-OCT-2003
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Q8N4Y9;
01-OCT-2002
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01-OCT-2002 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.;
Hypothetical protein.
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Homo sapiens (Human).
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUN-2002) to the EMBL; BC033178; AAH33178.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Primary B-Cells;
Strausberg R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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                                                                                                                                                                                             KMYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                         EPKSCDTPPPCPRCPAPELLGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVQF
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                                                                                                      PMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPG
                                                                                                                 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                ISKTKGOPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESSGOPENNYNTTP
                                                                                                                                                             ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPG
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 (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                      Conservative
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                                              PRELIMINARY;
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Last sequence update)
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                                                                                                                                                                                                                                                                                    Score 1167; DB 4; Pred. No. 2.4e-80; 9; Mismatches 9;
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Catarrhini; Hominidae;
                                              PRT;
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RESULT P79355

19

SEE

P79355 P79355; 01-MAY-1997 01-MAY-1997

PRELIMINARY; (TrEMBLrel. (TrEMBLrel.

03,

Created)
Last sequence update)

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Best Local Sim:
Matches 260;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGy; 1.
PROSITE; PS00196; COPPER BLUE; 1
PROSITE; PS00196; COPPER BLUE; 1
PROSITE; PS00196; COPPER BLUE; 1
PROSITE; PS00196; IG_MHC; 3.
Hypothetical protein.
SEQUENCE 473 AA; 51986 MW; E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; BC025985; AAH25985.1; -.
GO; GO:0005507; F:copper ion binding; IEA.
GO; GO:0005489; F:electron transporter act
GO; GO:0006118; P:electron transport; IEA.
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454
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              MHEALHNHYTQKSLSLSPG
                                                                   LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
                                                                                                                     VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTC
                                                                                                                                                                                                                 VVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFLFPPKP
                                                                                                                                                                                                                                                                                                                                                                                                      GEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMG
                                                                                                                                                                                                                                                                                                                                                                                                                                  LSRLQLQESGPGLLKPSVTLSLTCTVSGD---
MHEALHNHYTQKSLSLSLG
                                                   LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSV
                                                                                                      VLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTC
                                                                                                                                                           KDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLT
                                                                                                                                                                              KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT
                                                                                                                                                                                                                                          IKVLPTWSTPVEPKSCDKTH-------TCPPCPAPELLGGPSVFLFPPKP
                                                                                                                                                                                                                                                                      FPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL-SS
                                                                                                                                                                                                                                                                                               SPKLMLSLKLENKEAKVSKREK-----PVWV-----LNPEAGMWQCLLSDSGQVLLESN
                                                                                                                                                                                                                                                                                                                       ----SVTAADTAVYYCAAGHLVMGFGAHWG----QGKLVSVSPASTK------GPSV
                                                                                                                                                                                                                                                                                                                                                   KKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPT-
                                                                                                                                                                                                                                                                                                                                                                              GKGLEWIGTINF-----SGNMYY----SPSLRSRVTMSADMSENSFYL-----KLD--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.7%; 52.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to the EMBL/GenBank/DDBJ
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%; Pred. No. 4.2e:
43; Mismatches
                          625
 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity;
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1.2e-79;
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Best Local Simi
Matches 239;
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Norinine J., Miyazawa T., Kawaguchi Y.
"A cDNA encoding feline CD4 has a union the V-like region.";
Immunology 75:74-79(1992).
EMBL; AB000483; BAA19124.1;
HSSP; P01730; 1WIQ.
Q61396;
Q61396;
01-NOV-1996
01-NOV-1996
01-OCT-2003
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SIGNAL
CHAIN
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PROSITE; PS50835; IG_LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0016020; C:membrane; IEA.
GO; GO:0006955; P:immune response;
InterPro; IPR000973; CD4 TCAg.
InterPro; IPR007110; Ig-like.
InterPro; IPR00756; Ig_v.
Pfam; PF00047; 1g; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. Miyazawa T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CD4 antigen precursor.
Felis silvestris catus (Cat).
Eukaryota, Metazoa, Chordata; (
Mammalia; Eutheria; Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Miyazawa
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                                                                                        LKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNIKVLP----TWS
                                                                                                                        LTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLS
                                                                                                                                              SPPLNPEDENLMGN--LRWKAEGAPSSLLWISFTLKNKQLSVKEVDPYSKLQMMDSLPLR
                                                                                                                                                          SFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLH
                                                                                                                                                                                                                  QLLVFGLTANSD------THLLQGQSLTLTLESPPGSSPSVQCRSPRGK
                                                                                                                                                                                                                                                             KILGNQGSFL-TKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEV
                                                                            LKLKGQAAKVSKQQKMVRVEDAEAGTWQCLLSHKDKVLLASKAEVLPPVLTRTWT
                                                                                                                                                                                                                                                   KILESQHSSLCLTGSSKLKTRFESKKILWDQGSFPLVIKSLQVADSGIYTCEVENKKREV
                                                                                                                                                                                                                                                                                     MNQGAVERHLLLVLQLVMLKAAVPQGKEVVLGKAGGTABLPCQASQKKYMTFTWRLSSQV
                                                                                                             FTLPNVLSRYAGSGNLTLVLD--KGQLQQEVKLVVMRVTQSGNNLTCEVLGPTSPELTLS
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27
474 AA;
(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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474
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Last annotation updat
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Pred. No. 2
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la; Felidae;
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update)
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RESULT 21
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O55054, OTTEMBLEEL. 0
O55054, OTTEMBLEEL. 0
O1-JUN-1998 (TREMBLEEL. 0
O1-OCT-2003 (TREMBLEEL. 2
T4 surface glycoprotein (CD4.
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Query Match
Best Local S
Matches 210
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GG; GG:0016020; C:membrane; IEA.
GG; GG:0006955; P:immune response; IE
InterPro; IPR000973; CD4_TCA9.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 2.
PRINTS; PR00692; CD4TCANTIGEN.
SMART; SM00406; IGv; 1.
SMCRT; PS50835; IG LIKE; 1.
SEQUENCE 457 AA; 51368 MW; 24AB19
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EMBL; M17080; AAA37402.1; JO

EMBL; M17076; AAA37402.1; JO

EMBL; M17077; AAA37402.1; JU

EMBL; M17078; AAA37402.1; JU

EMBL; M17079; AAA37402.1; JU

EMBL; M17079; AAA37402.1; JU

HSSP; P01730; IWBR.

MGD; MGI:88335; Cd4.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gorman S.D.,
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356
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                                                                                        NLTLALEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKRE
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                                                                                                                                                                                                           VQDSDFWNCTVTLDQKKNWFGMTLSVLGFQSTAITAYKSEGESAEFSFPLNFAEE--NGW
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                                                                                                                                                                                                                                                                                                          EVQLLVFGLTANSDTHLLQGQSLTLTLES-PPGSSPSVQCRSPRGKNIQGGKTLSVSQLE
KVVQVVAPETGLWQCLLSEGDKVKMDSRIQVL
                               KPVWVLNPEAGMWQCLLSDSGQVLLESNIKVL
                                                                    NLTLTLD--KGTLHQEVNLVVMKVAQLNNTLTCEVMGPTSPKMRLTLKQENQEARVSEEQ
                                                                                                                                         GELMWKAEKDSFFQPWISFSIKNKEVSVQKSTKDLKLQLKETLPLTLKIPQVSLQPAGSG
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Tourvieille B., Parn
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Rodentia;
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Sciurognathi; Muridae;
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; Murinae; Mus
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RESULT 22
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GG; GO:0016020; C:membrane; IEA.
GG; GO:0005955; P:immune response; IE
InterPro; IPR00973; CD4 TCA9.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 2.
PRINTS; PR00692; CD4TCANTIGEN.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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                    Q95M34;
Q95M34;
01-DEC-2001
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SEQUENCE
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01-DEC-2001 (TremBLrel. 19, 01-DEC-2001 (TremBLrel. 19, 01-OCT-2003 (TremBLrel. 25, Immunogobulin gamma 1 heavy
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MEDLINE=88097446;
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Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structure and expression of the human and mouse Proc. Natl. Acad. Sci. U.S.A. 84:9155-9159(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                              TQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVL
                                                                                                                                                                                                                                                                                                                                                                                                                                 EVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRA
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Eutheria;
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433 AA;
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                                                                                                                 PRELIMINARY;
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neaux S.M., Maddon
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Rodentia;
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Created)
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chain constant region (
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Sciurognathi; Muridae;
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; Murinae; Mus
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Best Local &
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SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG_LIKE; 3
PROSITE; PS00290; IG_MHC; 2.
NON_TER
                                                                                                                                                                            Hypothetical protein.
Mus musculus (Mouse).
Bukaryota; Metazoa; Ch
Mammalia; Eutheria; Ro
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                        Q7TMK1;
Q7TMK1;
01-OCT-2003
01-OCT-2003
01-OCT-2003
SEQUENCE FROM N.A.
STRAIN-CZECH II; TISSUE-Breast tumor;
MEDLINE-22388257; PubMed=12477932;
MEDLINE-22388257; Peingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G
Rlausner R.D., Ceberg B., Buetow K.H., Schaefer C.F., Bhat N.K
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunobiology 199:105-119(1998).
EMBL; AJ300675; CAC44624.1; -.
InterPro; IPR0071110; Ig-like.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003006; Ig_MHC.
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Leibold W., Radbruch A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wagner B.;
Submitted (DEC-2000)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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ch G., Sheoran A.,
                                                                                                                                                                                                       Chordata;
Rodentia;
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Ig_cl.
Ig_MHC.
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Last annotation updat
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3; Mismatches
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                                                                                                                                                                                                       Craniata; Vertebrata; | Sciurognathi; Muridae;
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                                                                                                                                                                                                          Euteleostomi;
; Murinae; Mus
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Best Local :
Q9R1A4;
Q9R1A4;
01-MAY-2000
01-MAY-2000
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bossk S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases EMBL; BC055910; AAH55910.1; -. Hypothetical protein. SEQUENCE 470 AA; 51727 MW; 6D90E4DF896BB090 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CZECH II; TISSUE-Breast
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                                                                                       24
                                                                                                                                 426
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                                                                                                                        TYPLYSKLTVDTDSWLQGEIFTCSVVHEALHNHHTQKNLSRSPG
                                                                                                                                             SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                    PVTVKWNYGALSSGVRTVSSVLQSGFYSLSSLVTVPSSTWPSQTVICNVAHPAS-----
                                                                                                                                                                                                                                                                                                                     THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGV
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                                                                                                                                                                                                                                                                                                      ----SCPPGNILGGPSVFIFPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNK
                                                                                                                                                                                                                                                                                                                                                                                           LKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVEPKSCDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----TGKLHQEVNLV-------VMRATQLQKVLTCEVWGPTSPKLMLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WGAGTTVTVSSAT------TTAPSVYPLVPGCGDTSGSSVTLGCLVKGYFPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --KNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSG-----NLTLALEAK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGASVKISCKA-SGYTFTGYYMHWVKQSHGKSLEWIGLVNPSNGDTS----YNQK---FK
                                                                                                                                                                                                                                                                                                                                                                  -----KTELIKRIEP-----
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(TrEMBLrel.
(TrEMBLrel.
(TrEMBLrel.
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                                                          PRELIMINARY;
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 35,25
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Created)
Last sequence update)
Last annotation updat
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Pred. No. 8.
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.6e-57;
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update)
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                                                                                                                                                            625
                                                                                                                               469
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Best Local S
Matches 202
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SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 1.

NON_TER 1 1

NON_TER 437 437
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PIR; B45837; B45837.
PDB; 1CQK; 11-SEP-99.
PDB; 1191; 25-DEC-02.
PDB; 1KCU; 11-MAY-02.
MGD; MGI:96446; Igh-4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003056; Ig_V.
Pfam. PEP00477: G: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.; "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single chain antibody (scFV).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gammal heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
372
                                                                                                                                          441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 LGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
           ESNGQPENNYKTTPPYLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
                                                                                                                                                                     NIKVLPTWSTPVEPKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC
-----IVPRDCG----CKPCICTVPEV---SSVFIFPPKPKDVLTITLTPKVTC
                                                                         KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW
                                                                                                                             VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
                                                                                                                                                                                                                               SETVTCNVAHPAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDKDRNILSLQMSSLRSEDTAMYYC
QWNGQPAENYKNTQPIMDTDGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKNL
                                                       RVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEW
                                                                                                                                                                                                                                                         QKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLES
                                                                                                                                                                                                                                                                                       -----VH-TFPAVLQSDLYTLSSSVT-----VPSSTWP
                                                                                                                                                                                                                                                                                                                RVTQDPKLQMGKKLPLHLTLPQALPQ--YAGSGNLTLALEAKTGKLHQEVNLVVMRATQL
                                                                                                                                                                                                                                                                                                                                                                         QKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSVK
                                                                                                                                                                                                                                                                                                                                                                                                     AAKTTPPSVYPLAP-----GSAAQTNSMVTL------------
                                                                                                                                                                                                                                                                                                                                                                                                                                   SPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVKPGGSLKLSCAASGFTFSSYAMSWVRQTPEKRLEWVASFSSGGIIYYTDSVKGRFTIY
                                                                                                               VVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKC
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437 AA; 48142 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                               GCLVKGYFPEPVTVT
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                                                                                                                                                                                                                              -----STKVDKK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74;
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431
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Best Local Similarity
Matches 189; Conserv
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InterPro; IPRO03006; Ig-MHC.
InterPro; IPRO03096; Ig-v.
IfterPro; IPRO03996; Ig-v.
IfterPro; IPRO03996; Ig-v.
IfterPro; ISSO0406; IGv; 1.
ISSO04176; ISSO0406; IGv; 1.
INTERPOSITE; PS00290; IG-MHC; 1.
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OBR3V9;

OLJUN-2002 (TREMBLIEL 2

OLJUN-2002 (TREMBLIEL 2

OLOCT-2003 (TREMBLIEL 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; BC024405; AAH24405.1;
PIR; B45837; B45837.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (MAR-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
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                                                 NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN
                                                                                                      DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS
                                                                                                                                                                    VLPTWSTPVEPKSCDXTHTCPP--CPAPELLGGPSVFLFPPXPXDTLMISRTPEVTCVVV 443
GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
                             SAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWN
                                                                                        DISKDDPEVQFSWFVDDVEVHTAQTKPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVN
                                                                                                                                                 -----IVPRDCG----CKPCICTVPEV---SSVFIFPPKPKDVLTITLTPKVTCVVV
                                                                                                                                                                                                                                       LTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNIK 385
                                                                                                                                                                                                                                                                    -----FPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSQT
                                                                                                                                                                                                                                                                                                  KLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEV-----NLVVMRATQLQKN 325
                                                                                                                                                                                                                                                                                                                                 TVSAAKTTPPSVYPLA-----PGS-----AAQTNSMVTLGCLVKGY-----
                                                                                                                                                                                                                                                                                                                                                            EFS-----FPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSVKRVTQDP 270
                                                                                                                                                                                                                                                                                                                                                                                          RDNSQSILYLQMNALRAEDSATYYCA---RDRRSSY-----YYSGTSFAYWGQGTLV 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGGSLRLSCAASGFTFTDYYMSWVRQPPGKALEWLGFIRNKANGYTTEYSASVKGRFTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGSSPSVQC-----NIQGGKTLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    625
                                                                                                                                                                                                                                                                                                                                                                                                                      -VSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.9%; Score 850.5;
34.9%; Pred. No. 2.7e
tive 75; Mismatches
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      534793F155D05457 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.7e-56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109;
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; Murinae; Mus
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RESULT

Q99LC4

AC Q99
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig; 3.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 4.

PROSITE; PS00290; IG MHC; 1.

SECULENCE 463 AA; 51007 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JCT-2003 (TrEMBLrel. 25, Last annotation updat
Similar to RIKEN cDNA 1810060009 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q99LC4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q99LC4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; B45837; B45837.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BC003435; AAH03435.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (FEB-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:96446; Igh-4
InterPro; IPR007110;
InterPro; IPR003006;
InterPro; IPR003596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IGH-4
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                                         RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 593
                                                                                                                                                                                                            LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    გ<u>—</u>გ
                                                                                                                                      QYNSTYRVVSYLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GOSTTLTLESPPGSSPSVQCRSPRGK-NIQGGKTLS-----VSQLELQDSGTWTCTVLQN
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KEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFIYSKLNVQK
                                                                                                       QFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPP
                                                                                                                                                                                                                                                                                                                                                                           KPVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVEPKSCDKTHTCPP--CPAPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                   VHTFPAVLQSDLYTLSSSVTVPSSTWPSETVTCNVAHPAS-----STKVDKK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEAKTGKLHQEV-----NLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----AAQTNSMVTLGCLVKGY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -RSSYYSYDL-----FAYWGQGTLVTVSAAKTTPPSVYPLA-----PGS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFS-----FPLAFTVEKLTGSGELWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GQGLEWVGEIYPGSGNTYYSEKFKGKATLTTDKSSSTAYMHLSSLTSEDSAVYFCA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ig-like.
ig_MHC.
ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.7%;
36.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 844; DB 11;
Pred. No. 8.2e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EAA674C6BBC30783 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 120;
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RC STRAIN=C57BL/60; TISSUE=Pancreas;

RX MEDLINE=21085660; PubMed=11217851;

RX MEDLINE=21085660; PubMed=11217851;

RX Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishi Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kasukawa T., Saito R.,

RA Arakawa T., Hara A., Fukunishi Y., Sasukawa T., Saito R.,

RA Arakawa T., Hara A., Fukunishi Y., Sasukawa T., Saito R.,

RA Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gaeriboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 208
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Q9DBL4;
Q9DBL4;
Q9DBL4;
Q1-JUN-2001 (TrEMBLrel. 17, C
Q1-JUN-2001 (TrEMBLrel. 17, L
Q1-QCT-2003 (TrEMBLrel. 25, I
Q10060009Rik protein.
Q1-1 OR 1810060009RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; 1g; 3.

SMART; SM004406; 1Gv; 1.

PROSITE; PS50035; IG_LIKE; 4.

PROSITE; PS00250; IG_MIC; 1.

SEQUENCE 473 AA; 51699 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AK007918; BAB25349.1; -.
PIR; S26746; S26746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4SSP; P01842; 7FAB.
MGD; MGI:96443; Igh-1.
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                                                                                                                                                                                                                                                                RSLW----DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANS----DTHLLQG
                                                                                                                                                                                                                                                                                                                           LVKPGASVKISCKASGYTFTDYY---INWVKORPGOGLEWIGKIGPGSGSTYYNEKFKGK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPG
IDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDL
                                                                                                                                QSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFK
                                                                                                                                                                                              ATLTADKSSSTAYMQLSSLTSEDSAVYFC-------ARSGYDYDWFAYWG
                                                              QGTLVTVSAAKTTAPSVYPLAP----VCGGTT------
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 840.5; D
Pred. No. 1.6e-
75; Mismatches
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9DED57A514475FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; DB 11; Length 473; .6e-55;
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Q9913
ID Q9913
AC Q9913
AC Q9913
DT 01-UU
DT 01-OC
DE SIMIN
OC BUKBR
OC MUBMI
OC MAMMA
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                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 217
                                                                                                                                                                                                                                                                                                                                                                                                                           PHAM; PF00047; 1g; 3.

PHAM; PF00047; 1g; 3.

SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 1.

SEQUENCE 468 AA; 51661 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q99L31 PRELIMINARY; PRT; 468 AA. Q99L31; 01-JUN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Similar to RIKEN cDNA 1810060009 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BC003878; AAH03878.1; PDB; 2AP2; 24-NOV-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                  Local Similarity
les 217; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   464
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SLILILESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKI 197
                                                                             DKATITADTSSNTAY-LOLSSLTSEDTAIYYC-----ARNLLYG-----GYYDYWGO
                                                                                                                                                                                                                                  LGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKILGNQG-
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                                                                                                                                            DRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQ 137
                                                                                                                                                                                                 LVRPGASVKLSCTASGENIKDSLMHW-----VKQRPEQGLEWIGWIDPEDGETKYAPKFQ
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                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                            24.4%; Score 832; DB 11; 35.5%; Pred. No. 6.8e-55; tive 65; Mismatches 140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 96352328B3332ADB CRC64;
                                                                                                                                                                                                                                                                                                                                                                     Length 468;
                                                                                                                                                                                                                                                             -----SFLTKGPSKLN
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                                                                                                     Query Match
Best Local Similarity
Matches 165; Conserv
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Q99L25;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to RIKEN CDNA 1810060009 gene.
Mus musculus (Mouse).
                                                                                                                                                                                            InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 3.
SMART; SM00406; IGv; 1.
                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (FEB-2001) to the
EMBL; BC003888; AAH03888.1;
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               456
                                                                                                                                                      PS50835; IG_LIKE; 4.
PS00290; IG_MHC; 1.
473 AA; 52449 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:| || |:||
HHTTKSFSRTPG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSPMVTCVVVDVSEDDPDVQISWFVNNVEYLTAQTQTHREDYNSTLRVVSALPIQHQDWM
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                       LSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVEPKSC
                                                  PEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPAS----
                                                                         PQALPQYAGSGNLTLALEAKTGKLHQEV-----NLVVMRATQLQKNLTCEVWGPTSPKLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYTOKSLSLSPG 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTSSTWPSQSITCNVAHPAS-----STKVDKKIEP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQ--YAGSGNLTLALEAKTGKLHQEVNLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTTITVSSAKTTAPSVYPLAP----VCGDTT-------
                                                                                                  23.7%; Score 810.5; DB 11; Length llarity 47.4%; Pred. No. 3e-53; Conservative 47; Mismatches 77; Indels
STKVDKKIEP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GSSVTL---GCLVKGYFP-----EPVT----LTWNSGSLSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----VH-TFPAVLQSDLYTLSSSVT-----
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                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                         BE9889B7986DA155 CRC64;
                                                                                                                             DB 11; Length
                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
; Murinae; Mus.
PT---- IKP---
                                                                                                   59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUL-2001) to the EMBL/GenBank/DDBJ day
EMBL; BC010327; AAH10327.1; -.

MGD; MGI:2144967; AU044919.

GO; GO:0005489; F:electron transporter activity;
GO; GO:0006118; P:electron transport; IEA.

InterPro; IPR000345; CYCC heme_BS.

InterPro; IPR007110; Ig-like.

InterPro; IPR00306; Ig_MHC.

InterPro; IPR00306; Ig_MHC.

InterPro; IPR00356; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; 19; 3.

SMART; SM00406; IGv; 1.

PROSITE; PS00190; CYTTOCHROME_C; 1

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 1.

Hypothetical protein.

SEQUENCE 473 AA; 51946 MM; CF6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q91Z05;
Q91Z05;
01-DEC-2001
01-DEC-2001
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
AU044919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                       LGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKILG----NQGSF-----LTKGPSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
KNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVV
                                                                                                                                                                                               QSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFK 196
                                                                                                                                                                                                                                               S-RDNAKNTLF-----LOMTSLRSEDTAMYYCARELWLRRID----
                                                                                                                                                                                                                                                                                              NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG
                                                                                                                                                                                                                                                                                                                                                 LVKPGGSRKLSCAASGFTFSDYGMHWVRQAPEKGLEWVAYINSGSTTIYYADTVKGRFTI 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPG
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                                                                                               IDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDL
                                                                                                                                               QGTTITVSSAKTTPPSVYPLAPGCGDTTG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Chordata;
; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51946 MW; CF625F008932AF12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.4%;
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19,
25,
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 800.5; DB 11; Length Pred. No. 1.7e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     473
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databa
EMBL; BE025447; AAH25447.1; -.

RMGD; MGI:2144967; AU044919.

GO; GO:0005489; F:electron transporter activity; IEA
GO; GO:0005118; P:electron transport; IEA.

RINterPro; IPR000345; CytC heme_BS.

RINterPro; IPR000306; Ig_MHC.
RINterPro; IPR003006; Ig_MHC.
RINTERPro; IPR003096; Ig_MHC.
                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002
01-JUN-2002
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00190; CYTOCHROME_C; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50290; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 474 AA; 51748 MW; 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; ig; 3
SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8R3H6
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                                                                                                                                                                                                                                           209;
                                               71
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                                                                                                                                                                                                                                                                  Similarity
EEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLE
                                                                                                                                            OVOLLOSGPE----LVKPGASVKISCRASGYAFSKS----WMNWVKRRPGKGLEWIGRI
                                                                                                                                                                                       QLALLPAATQGNKVVLGKKGDTVELTCTASQ---KKSIQFHWKN-----SNQIKILGN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTIRVVSALPIQHQDWMSGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
                                             FPGDGDTHYSGKF--QGKAKLTADKSSVTAF-----LQLTSLTSEDSAVYFCARDSD-
                                                                                          -----QGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QKSLSLSPG 625
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2 (TrEMBLrel.
3 (TrEMBLrel.
                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                      23.4%; Score 799.5; DB: 33.2%; Pred. No. 2.1e-52 ative 71; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                   51748 MW; 8608B57C6CD2874A CRC64;
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Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                         Mismatches 155;
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                                                                                          Query Match
Best Local S
Matches 151
                                                                                                                                                                                    InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 5.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS00290; IG_MHC; 3.
Hypothetical protein.
SEQUENCE 613 AA; 67273 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (JUL-2001) to the
EMBL; BC011857; AAH11857.1;
PIR; S15590; S15590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein. Homo sapiens (Human).
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01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   096EY0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=B-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                   Similarity
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KHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPAG
                                          RHLLLVLQLALLP-----AATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKI 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NSTIRVVSALPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYILPPPAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
Primates;
                                                                                                                                                                                         67273 MW;
                                                                                                                12.2%;
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Last annotation updat
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                                                                                          Score 417.5; DB Pred. No. 3.7e-23.7; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                         31214203FB8421E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   613
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                                                                                                                                       DB 4;
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Hominidae; Homo.
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                                                                                          Indels
                                                                                                                                    Length
                                                                                                                                         613;
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61
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RA Staubers M.B., Jordan H., Schaefer C.F., Bhat N.K., RA Diatchenko L., Marusina K., Farmer A.A., Robin G.M., Schuler T.E., RA Brownstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C., RA Rabes S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
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Hypothetical )
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISKAKGQP-REPQVYTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENN
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Rodentia;
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annotation update)
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Best Local S
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Jones S.J., Marra M.A.;
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein. SEQUENCE 614 AA; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUN-2003) to the EMBL; BC053409; AAH53409.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=C57BL/6NCr; TISSUE=Hematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
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TVDKS-
                                                                                                            LLQGQSLTLTLESP--PGSSPSVQCRSP-RGKNIQGGKTLSVSQLELQDSGTWTCTVLQN
                                                                                                                                                                                              DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --QGTLVTVSAESQSFPNVFPLVSCESPLSDKNLVAMGCLARDFLPSTISFTWN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKLN-DRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGKKGDTVELTCTASQKKSIQFHWKN-----SNQIKILGN------QGSFLTKGP
                          SLSISPGLQLDETCAEAQDGELDGLWTT
                                                       RGQLLPQEKYVTSAPMPEPGAPGFYFTHSILTVTEEEWNSGETYTCVVSHEALPHLVTER
                                                                                 NGQ--PENNYKTTPPVLD--SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK
                                                                                                                                                                     E-TLNISWASQSGEPLETKIKIMESHPNGTFSAKGVASVCVEDWNNRKEFVCTVTHRDLP
                                                                                                                                                                                                                                                       TWSTPVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
                                                                                                                                                                                                                                                                                  ESGFTTDPVTIENKGSTPQTYKVISTLTISEIDWLNLNVYTCRVDHRGLTFLK-----
                                                                                                                                                                                                                                                                                                              KVSKREKPVWVLN----PEA--
                                                                                                                                                                                                                                                                                                                                                                   NLTLALEAKTGKLHQEVNLVV-----MRATQLQKNLTCEVWGPTSPKLMLSLKLENKEA
                                                                                                                                                                                                                                                                                                                                                                                               TFPTLRTGGKYLATSQVLLSPKSILEGSDEYLVCKIHYGGKNKDLHVPIP
                                                                                                                                                                                                                                                                                                                                                                                                                         SWITFDLKNKEVSVKRVTQDPKLQM-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATLTADKSSSTAYMQ------LSSLTSEDSAVYFC-ARDYGSSYRFAYWG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative 101; Mismatches 233;
                                                                                                                                                                                                                                                                                                                                        ---AVAEMNPNVNVFVPPRDGFSGPAPRKSKLICEATNFTPKPITVSWLKDGKLV
 -TEGEVNAEEEGFENLWTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67746 MW;
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22.7%;
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No. 4.
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                                                                                                                                                                                                                                                                                                             -GMWQCLLSDSGQVLLESNIKVLP
                                                                                                                                                                                                                                                                                                                                                                                                                         -GKKLPLHLTLPQALPQYAGSG
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RESULT Q8WUK1 ID Q8

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Q8WUK1

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Best Local Similarity
Matches 150; Conserv
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01-MAR-2002
01-MAR-2002
01-OCT-2003
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 5.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical
SEQUENCE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50835; IG_LIKE; 5. PROSITE; PS00290; IG_MHC; 3.
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PIR; S15590; S15590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (DEC-2001) to the EMBL; BC020240; AAH20240.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein. Homo sapiens (Human).
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FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGELDG
                                                                                                                                                                                                                                                                                                                                                                                                                          HLLQGQSLTLTLESPPGSSPS----VQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVL 187
                                     YLLPPAREQLNLRESATITCLVTGFSPADVFVQMMQRGQPLSPEKYVTSAFMPEPQAPGR
                                                                                        NISESHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDV
                                                                                                                                                                                                                                            SKLICOATGESPRQIQVSWLREGKQVGSGVTTDQVQAEAKESGPTTYKVTSTLTIKESD-
                                                                                                                                                                                                                                                                    TLALEAKTGKLHQEVNLVVMR-----ATQLQKNLTCEVWGPTSPKLMLSLKLENKEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT
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                                                    YTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGS
                                                                                                                KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQV
                                                                                                                                                                  PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
                                                                                                                                                                                                                   KVSKREKPVWVLNPEAGMWQCLLSDSGQVLLE-SNIKVLPTWSTPVEPKSCDKTHTCPPC
                                                                                                                                                                                                                                                                                               ------MQGTDEHVVCKVQHPNGNKEKNVPLPVIAELPPKVSVFVPPRDGFFGNPRK
                                                                                                                                                                                                                                                                                                                      SSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHL--TLPQALPQYA-----
                                                                                                                                                                                                                                                                                                                                                                                                   FDIWGQGTMVTVSSGSASAPTLFPLVSC-----
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613 AA; 6
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(TrEMBLrel.
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                                                                                                                                         VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHT
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Primates;
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22.6%; Pred. No. 2.1
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60C7F5950671E315 CRC64;
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.es 252; Indels 143;
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RESULT 36
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Best Local Similarity
Matches 76; Conserv
                                                                                                                    O77597 PRELIMINARY;
O77597;
O17-NOV-1998 (TrEMBLrel. 08, C;
O1-NOV-1998 (TrEMBLrel. 28, L;
O1-OCT-2003 (TrEMBLrel. 25, L;
T-cell surface glycoprotein C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Fragment).

Wandrillus sphinx (Mandrill) (Papio sphinx).

Wandrillus sphinx (Mandrill) (Papio sphinx).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithe

Cercopithecinae; Mandrillus.

NCBI_TaxID=9561;
(Fragment).
Mandrillus leucophaeus (Drill) (Papio leucophaeus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Butheria; Primates; Catarrhini; Cercopith
Cercopithecinae; Mandrillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Nuclear gene trees and the phylogenetic relationships of the mangabeys (primates: Papionini).";
MO1. Biol. Evol. 15:892-900(1998).
-i- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O77596;
01-NOV-1998 (TrEMBLrel. 08,
01-NOV-1998 (TrEMBLrel. 08,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF057386; AAC25130.1; -. HSSP; P01730; 1CDY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY)
-i- SIMILARITY: BELONGS TO THE IMMUNOCLOBULIN SUPERFAMILY. CONTAI)
ONE V-LIKE AND 1 C2-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98320644; PubMed=9656488; Harris E.E., Disotell T.R.;
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                                                                                                                         Last sequence update)
Last annotation update)
CD4 (T-cell surface antigen
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Last annotation updat
CD4 (T-cell surface a
                                                                                                                                                                                                         Created)
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Pred. No. 4.8e-23;
5; Mismatches 3;
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RESULT 37
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Best Local
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-1- SUBURIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAIN:
ONE V-LIKE AND 1 C2-LIKE DOMAIN.
EMBL; AF057387; AAC25131.1;
-1- GO; GO:0016027
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01-NOV-1998
01-NOV-1998
-!- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMIL-
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
ONE V-LIKE AND 1 C2-LIKE DOMAIN.
EMBL; AF057381; AAC25125.1; -.
HSSP; P01730; 1CDY.
GO; GO:0016021; C:integral to membrane; IEA.
Interpro; IPR007110; Ig-like.
Immunoglobulin domain; T-cell; MHC; Transmembrane.
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DOMAIN
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MO1. Biol. Evol. 15:892-900(1998).
-i- FUNCTION: ACCESSORY PROTEIN FOR MHC
RECEPTOR INTERACTION. MAY REGULATE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=98320644; PubMed=9656488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Cercopith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cercopithecus mitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=98320644; PubMed=9656488;
Harris E.E., Disotell T.R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel.
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Last annotation update)
CD4 (T-cell surface antigen
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Pred. No. 4.8e-23;
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DOMAIN
                                                                                                                                    Immunoglobulin domain;
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MO1. Biol. Evol. 15:892-900(1998);
-i-FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-98320644; PubMed=9656488;
Harris E.E. Disotcell T.R.;
"Nuclear gene trees and the phylogenetic
                                                                                                                                                                                                                                                                                                                                                                        077599;
01-NOV-1998
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Mammalia; Eutheria; Primates; Catarrhini; Cercopitho
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9565;
                                                                                                                                                                                                                                                                                                          Cercopithecinae;
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                               RILSVPQLERQDSGTWTCTVSQDQK
RTLSVPQLERQDSGTWTCTVSQDQK
              KILSVSQLELQDSGTWICTVLQNQK
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n; T-cell; MHC; Transmembrane.
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Last annotation update)
CD4 (T-cell surface antigen
                                                              Score 397; DB Pred. No. 8.2e 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         Created)
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                                                                                                             IG-LIKE V-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 397; DB 6;
Pred. No. 8.2e-23;
5; Mismatches 4
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                                                                      DB 6;
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InterPro; IPR003006; Ig_MC.
InterPro; IPR003596; Ig_v.
Pfam; PF000407; Ig; 5.
SMART; SM00406; IGv; 1.
PROSITE; PS00290; IG_MIC; 3.
Hypothetical protein.
SEQUENCE 613 AA; 67855 MW;
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Q8VCX7;
01-MAR-2002
01-MAR-2002
01-OCT-2003
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Submitted (DEC
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 HRDLPSPQKKFISK----PNEVHKHPPAVYLLPPAREQLNLRESATVTCLVKGFSPADIS
                NKALPAPIEKTISKAKGQPRE-----PQVYTLPPSRDELT-KNQVSLTCLVKGFYPSDIA
                                                                    DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS
                                                                                                                                                                                                                                                                                                                                                        NSDTHLLQGQSLTLTLESP--PGSSPSVQCRSP-RGKNIQGGKTLSVSQLELQDSGTWTC
                                                                                                                                                                                                                                                                                                                                                                                         KATFTADTSSNTAYMO-----LSSLTSEDSAVYYC-----ARRLGRWYFDVWG---
                                              NLATYE-TLNISWASQSGEPLETKIKIMESHPNGTFSAKGVASVCVEDWNNRKEFVCTVT
                                                                                                                     IKVLPTWSTPVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV
                                                                                                                                                                     ENKEAKVSKREKPVWVLN----PEA-------GMWQCLLSDSGQVLLESN
                                                                                                                                                                                                                  YAGSGNLTLALEAKTGKLHQEVNLVV-----MRATQLQKNLTCEVWGPTSPKLMLSLKL
                                                                                                                                                                                                                                                                 ASSSKSWITFDLKNKEVSVKRVTQDPKLQM------
                                                                                                                                                                                                                                                                                                               TVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAER
                                                                                                                                                                                                                                                                                                                                         ----AGTTVTVSSESQSFPNVFPLVSCESPLSDKNLVAMGCLARDFLPSTISFTWN-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGKKGDTVELTCTAS------QKKSIQFHWKNSNQIKILGNQGS--FLTKGPS
                                                                                                                                             DGKLVESGFTTDPVTIENKGSTPQTYKVISTLTISEIDWLNLNVYTCRVDHRGLTFLK--
                                                                                                                                                                                             -----AVAEMNPNVNVFVPPRDGFSGPAPRKSKLICEATNFTPKPITVSWLK
                                                                                                                                                                                                                                           --GIRTFPTLRTGGKYLATSQVLLSPKSILEGSDEYLVCKIHYGGKNRDLHVPIP----
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(TrEMBLrel.
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SEPPPRE

Q96BB9; PRELIMINARY; Q96BB9; O1-DEC-2001 (TrEMBLrel. 1 01-DEC-2001 (TrEMBLrel. 1 01-DCT-2003 (TrEMBLrel. 2 01-OCT-2003 (TrEMBLrel. 2 Hypothetical procein. Homo sapiens (Human).

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                                                                                                                                                  Query Match
Best Local S
Matches 75
                                                                                                                                                                                                 077595
                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
-!- SUBCELLULAR LOCATION; TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
ONE V-LIKE AND 1 C2-LIKE DOMAIN.
EMBL; AF057382; AAC25126.1; -.
HSSP; P01730; 1CDY.
                                                                                                                                                                                                                                                                                                                                                                                                             mangabeys (primates: Papionini).";
Mol. Biol. Evol. 15:892-900(1998).
-!- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Cercocebus. NCBI_TaxID=75569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-OCT-2003 (TrEMBLrel. 25, T-cell surface glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harris E.E., Disotell T.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98320644; PubMed=9656488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cercocebus galeritus chrysogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Nuclear gene trees and the phylogenetic relationships
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Fragment).
                                                                                                                                                                                                                                                                                                        nterPro;
                                                                                                                                                                                                                                                                                                                 GO:0016021;
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                                                                                                                                                   1 Similarity 75; Conserv
                                                                                                               YICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG
                                                             KTLSVSQLELQDSGTWTCTVLQNQK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVTERTVDKS-----TEGEVNAEEEGFENLWTT
                                                 RTLSVPQLERQDSGTWTCNVSQDQK
                                                                                                  YICEVEDKKEEVELLVFGLTANSDTHLLEGQSLTLTLESPPGSSPSVKCRSPRGKNIQGG
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                                                                                                                                                                                                                                                                                                   16021; C:integral to membrane; IPR007110; Ig-like.
                                                                                                                                                   11.6%;
nilarity 88.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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Last annotation update)
CD4 (T-cell surface antigen
                                                                                                                                                   6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                  Score 395; DB 6;
Pred. No. 1.2e-22;
5; Mismatches 4
                                                 85
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RESULT 42
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Best Local Similarity
Matches 143; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015760; AAH15760.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003096; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 5.
SMART; SM00406; IGV; 1.
PROSITE; PS00835; IG_LIKE; 5.
PROSITE; PS00835; IG_LIKE; 5.
PROSITE; PS00830; IG_MHC; 3.
077598;
077598;
01-NOV-1998
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SEQUENCE 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=B-cel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
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                                                                                                                   KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                    SRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGSFFLYS
                                                                                                                                                                                                                                                                                                                                                                           QATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAKESGPTTYKVTSTLTIKESD-----
                                                                                               ILTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKSTG
                                                                                                                                                    AREQUILLESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHS
                                                                                                                                                                                                          HPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPP
                                                                                                                                                                                                                                     QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQVYTLPP
                                                                                                                                                                                                                                                               ----VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHTNISES
                                                                                                                                                                                                                                                                                           LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                                                                                                                                                      ----WL---SQSMFTCRVDHRGLTFQQNASSMCVPDQDTAIR-------
                                                                                                                                                                                                                                                                                                                                                EKPVWVLNPEAGMWQCLLSDSGQVLLE-SNIKVLPTWSTPVEPKSCDKTHTCPPCPAPEL
                                                                                                                                                                                                                                                                                                                                                                                                       AKTGKLHQEVNLVVMR-----ATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKR
                                                                                                                                                                                                                                                                                                                                                                                                                                 ---- MOGTDEHVVCKVOHĖNGNKEKNVĖLĖVIAELĖPKVSVFVPPRDGFFGNPRKSKLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QDFLPDSITFSWKYKNNSDISSTRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSLTLTLESPPGSSPS-----VQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S-RDNSRDTLYLQMN-----SLRAEDTAVYYCAKDPRG----YSASGNYTREDYWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVQPGGSLRLSCAASGFSFSSYAMNWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGKKGDTVELTCTAS--QKKSIQFHWKNSNQIK-----ILGNQGSFL----TKGPSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGTLVTVSSGSASAPTLFPLVSC--------ENSPSDTSSVAVGCLA
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597 AA; 6
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                            PRELIMINARY;
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Pred. No. 2.9e
16; Mismatches
                            PRT;
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RESULT 43
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Best Local
                                                                                                                                                                                                                                                                                          Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Cho
Mammalia; Eutheria; Pr
                                                                                                                                                                                                                                                                                                                                                                                   Q96GA6;
Q96GA6;
01-DEC-2001
01-DEC-2001
01-OCT-2003
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CARBOHYD
DISULFID
NON TER
SEQUENCE
                Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC009851; AAH09851.1; -.
PIR; S15590; S15590.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0003700; F:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000005; HTHARAC.
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01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
7-cell surface glycoprotein CD4 (T-cell surface ant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0016021; C:integral to membrane; IEA. InterPro; IPR007110; Ig-like. Immunoglobulin domain; Glycoprotein; T-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mangabeys (primates: Papionini), ",
Mol. Biol. Evol. 15:892-900 (1998).
-i-FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98320644; PubMed=9656488;
Harris E.E., Disotell T.R.;
"Nuclear gene trees and the phylogenetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                              Strausberg R.;
                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE=B-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF057388; AAC25132.1; HSSP; P01730; 1CDY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
-!- SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY)
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAI
ONE V-LIKE AND 1 C2-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=61183;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin domain;
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InterPro;
                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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>86
79
78
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Primates;
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Primates;
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87.1%;
Ig-like
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Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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Pred. No. 2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IG-LIKE V-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
N-LINKED (GLCNAC. . .)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A9D97A98574EE9BE
                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     sequence update) annotation updat
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RESULT 44
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Best Local Similarity 22.0
Matches 150; Conservative
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SMART; SM00406; IGV; 1
PROSITE; PS00041; HTH j
PROSITE; PS50835; IG LI
PROSITE; PS50835; IG LI
                                                     077601;
01-NOV-1998
01-NOV-1998
                           01-OCT-2003
T-cell surfa
                                                                                              077601
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Lophocebus albigena albigena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003006; Ig_MHC
InterPro; IPR003596; Ig_v.
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PS50835; IG_LIKE; 5.
PS00290; IG_MHC; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLE-SNIKVLPTW
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                                                                                                                                                                                          GLQLDETCAEAQDGELDGLWTT 646
                                                                                                                                                                                                                                                                          LKQTISRPKGVALHRPDVYLLPPAREQLNLRESATITCLVTGFSPADVFVQWMQRGQPLS
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                                                                                                                                                                                                                     PEKYVTSAPMPEPQAPGRYFAHSILTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKS-
                                                                                                                                                                                                                                              ENNYKTTPPVLD--SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
                                                                                                                                                                                                                                                                                                   IEKTISKAKGQP-REPQVYTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--
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                                        (TrEMBLrel.
                                                                 (TrEMBLrel.
                                                                                              PRELIMINARY;
                                                                                                                                                                TEGEVSADEEGFENLWAT
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22.0%; Pred. No. 5.5e-21;
tive 116; Mismatches 272; Indels
                                      . 08, Created)
. 08, Last seq
. 25, Last anno
                        Last sequence update)
Last annotation update)
CD4 (T-cell surface antigen T4/LEU-3)
                                                                                              PRT;
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RESULT 45
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Best Local S
Matches 74
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077600;
01-NOV-1998 (TrEMBLrel. 08,
01-NOV-1998 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                          (Fragment).
Loghocebus aterrimus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithe
Cercopithecinae; Lophocebus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE V-LIKE AND 1 C2-LIKE DOMAIN.
EMBL; AF057391; AAC25135.1; -.
HSSP; P01730; 1CDY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harris E.E., Disotell T.R.;
"Nuclear gene trees and the phylogenetic relationships of the mangabeys (primates: Papionin).";
MOI. Biol. Evol. 15:892-900(1998).
-!- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Lophocebus. NCBI_TaxID=75568;
                                                                                                                                                         MEDLINE=98320644; PubMed=9656488; Harris E.E., Disotell T.R.;
                                                                                                                                                                                                      NCBI_TaxID=75566;
                                                                                                                                                                                                                                                                                    T-cell surface glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0016021; C:integral to membrane;
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                                                                                                                                                                                  EQUENCE FROM N.A.
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SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAIN
ONE V-LIKE AND 1 C2-LIKE DOMAIN.
L; AF057390; AAC25134:1; -.
P; P01730; 1CDY.
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                                                                                  SIMILARITY)
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87.1%;
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                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
CD4 (T-cell surface ant
                                                                                                                                                                                                                                                                                                                           Created)
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IG-LIKE C2-TYPE DOMAIN
BY SIMILARITY.
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7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 388;
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                                            CONTAINS
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Q96AAA
ID Q96AA
AC Q96AA
AC Q96AA
AC 01-DE
DT 01-DE
DT 01-GC
DE Hypot
OS Homo
OC Eukar
OC Mamma
OX NCBI
RN [1]
RN [1]
RN [1]
RR SEQUE
RA SUBmi
DR EMBL;
DR Intes
DR SEAR;
DR SMARF;

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Best Local S
Matches 149
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Best Local (
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 5.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS00290; IG_MHC; 3.
Hypothetical protein.
SEQUENCE 618 AA; 67758 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunoglobulin
NON_TER 1
DOMAIN <1
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Q96AA6;
Q1-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
CARBOHYD
DISULFID
NON TER
SEQÜENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (NOV-2001) to the EMBL; BC017356; AAH17356.1; PIR; S15590; S15590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=Lymph;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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                                                                                   --ARVITRASPGTDGRYGMDVWGQGTTVTVSSGSASAPTLFPLVSC
                                                                                                             EVQLLVFGLTANSDTHL----LQGQSLTLTLESPPGSSPS-----VQCRSPRGKNIQGGKTL
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                                                                                                                                                                           KGLEWIGEINHSGSTNYNPSLKSRYTISVDTSKKQLSLKLSSVNAADTAVYYC-----
                                                                                                                                                                                                                                                                                                              RHLLLVLQLALLP-----AATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKI
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                                       SVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLAFQ-KASSIVYKKEGEQVEFSFPLAFT
                                                                                                                                                                                                                     LGNQ--GSFLTKGPSKLNDRADSRRSL-WDQGNFPLIIKNLKIEDSDT--YICEVEDQKE
                                                                                                                                                                                                                                                                 KHLWFFLLLVAAPRWVLSQVQLQQWGAGLLKPSETLSLTCGVYGGSFSGYYWSWIRQPPG
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-ENSPSDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 383; DB 6; Le
Pred. No. 9.5e-22;
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IG-LIKE C2-TYPE DOMAIN.
N-LINKED (GLCNAC. . .) (POTENTIAL)
BY SIMILARITY.
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Best Local S
Matches 145
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InterPro; IPR003006; Ig_MC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; 1g; 5.
SMART; SM00406; IGV; 1.
SMOSTTE; PS50835; IG_LIKE; 5.
PROSITE; PS50835; IG_MHC; 3.
Hypothetical protein.
SEQUENCE 597 AA; 65274 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chu
Mammalia; Eutheria; Pr
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01-JUN-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL, BC002963; AAH02963.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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KGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKKQLSLKLSSVNAADTAVYYC---
                                                LGNO--GSFLTKGPSKLNDRADSRRSL-WDQGNFPLIIKNLKIEDSDT--YICEVEDQKE 116
                                                                                                      KHLWFFLLLVAAPRWVLSQVQLQQWGAGLLKPSETLSLTCGVYGGSFSGYYWSWIRQPPG
                                                                                                                                                       RHLLLVLQLALLP-----AATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLQLDETCAEAQDGELDGLWTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENNYKTTPPVLD--SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
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                                                                                                                                                                                                             Conservative 115;
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                                                                                                                                                                                                                                                                                                                65274 MW; 2DAFA8FB7E055851 CRC64;
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21.9%;
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                          Score 378.5; DB 4
Pred. No. 3.3e-20;
5; Mismatches 274
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Q9BQBB;
Q1-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-OCT-2003 (TrEMBLrel. 2
                                       InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 5.
SMART; SM00406; IGV; 1.
SMOSITE; PS50835; IG LIKE; 5.
PROSITE; PS00290; IG_MHC; 3.
Hypothetical protein.
SEQUENCE 597 AA; 65300 MW;
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUB-Muscle, and Lymph;
Strausberg R.;
Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC006.180; AAH01872.1; -.
EMBL; BC00.1872; AAH01873.1; -.
HSSP; P01825; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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  Score 376.5;
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Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC019235; AAH19235.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; !
PROSITE; PS00290; IG_MIC; 3
Hypothetical protein.
SEQUENCE 588 AA; 64438 M
                                                                                                                                                                                                                                   Q86TT1 PRELIMINARY; PRT; 375 AA.
Q86TT1;
Q1-TIN-2003 (TrEMBLrel. 24, Created)
O1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Human full-length cDNA clone CSODD006YL02 of neuroblastoma
                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                               sapiens (Human)
                                                       SEQUENCE FROM N.A.
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                              SSUE=Neuroblastoma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IEKTISKAKGQP-REPQVYTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVTISWTRQNGEAVKTHTNISESHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVQLLVFGLTANSDTHL---LQGQSLTLTLESPPGSSPS----VQCRSPRGKNIQGGKTL
:: : | | | | | | | | | | | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEKYVTSAPMPEPQAPGRYFAHSILTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENNYKTTPPVLD--SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKQTISRPKGVALHRPDVYLLPPAREQLNLRESATITCLVTGFSPADVFVQWMQRGQPLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STPVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----ENSPSDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLAFQ-KASSIVYKKEGEQVEFSFPLAFT
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21.9%; Pred. No. 7.8
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                                                                                                                                  Craniata; Vertebrata;
Catarrhini; Hominidae
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ches 273;
                                                                                                                                    Hominidae;
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PARA SEE REA S
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Best Local S
Matches 84
                                                                                                                                                                                                                                                                                                                                                                                                         Q13969;
01-NOV-1996
01-JAN-1999
01-OCT-2003
CD4 protein
                                                                                                                                        SEQUENCE FROM N.A.

Zverev V.V., Blinov V.M., Nedospasov S.A.;

Zverev V.V., Blinov V.M., Nedospasov S.A.;

"Splice-mediated insertion of antisence and sence Alu repeats CD4 gene: identification of three exons of CD4 mRNA.";

Submitted (APR-1993) to the EMBL/GenBank/DDBJ databases.
                           SEQUENCE FROM N.A.
MEDLINE=95407135; PubMed=7676667;
MZVETEV V.V., Sidorov A.V., Nedospasov S.A., Ma
Udalova I.A., Andzhaparizde O.G., Blinov V.M.;
                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q13969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 3. —
SMART; SM00407; IGc1; 3.
PROSITE; PS50835; IG_LIKE;
PROSITE; PS00290; IG_MHC; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Neuroblastoma;
Li W.B., Gruber C., Jessee J., Polayes D.;
"Full-length cDNA libraries and normalization.
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ
EMBL; BX161420; CAD61894.1; -.
GG; GO:0046821; C:extrachromosomal DNA; IEA.
                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
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[2]
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  [Nucleotide sequence of
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G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -ENNYKTTPPVLD--SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
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(TrEMBLrel.
(TrEMBLrel.
(Fragment).
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                                                                                                                                                                                                                                                                                                                                                                    (Human).
                                                                                                                                                                                                                                                                                                                    Chordata;
Primates;
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    two exons
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 357.5; DB 4;
Pred. No. 6.8e-19;
1; Mismatches 110;
                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                        RX MEDLINE-2238257; PubMed=12477932;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Hahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Hahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Hahesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Raphylinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human

"Generation and initial analysis of more than 15,000 full-length human
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Matches 70; Conser
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Vopr. Virusol. 40:100-102(1995).

EMBL; X97579; CAA60883.1; -.

EMBL; S79267; AAB35273.1; -.

PIR; 160082; 160082.

HSSP; P01730; 1CDY.

GO; GO:0004872; F:receptor activity; IE

InterPro; IPR007110; Ig-like.

PROSITE; PS50835; IG_LIKE; 1.
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Q7TOR1;
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22341132; PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L.,
Richardson P.;
                                 and
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                                 mouse cDNA sequences."
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Last annotation update)
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SIGNAL 1 18 POTENTIAL. CHAIN 19 684 NOVEL ANTIGEN RECEPTOR.	c; Signal.		IGC1; 4.	047; ig; 6.	1006; IG_M	IPR003597; Iq	IPRO07110; Iq-like.	4872: F:recept	HSSP: P01842: ZMCG.	DTB. GROOMS. GROOMS.	B48195 1.	73 (1995)	c diversification in sharks.":	eceptor gene f		A.S.,	183140; PubMed=7877689;		BEFORE ENGL. M. D.	GEOTIENCE EBON N D			Ginqlymostoma.	omorphii; Galeoidea;	zoa; Chordata;	um (Nurse	receptor precursor.	2003 (TrEMBLrel. 25, Last	rEMBLrel. 01, Last sequence update)	rEMBLrel 01, Created)		090544 PRELIMINARY; PRT; 684 AA.			556 ESTANGET GREET		LHNHYTOKSLSLSPGLQLD		DIKDWDAG	 557 AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH 608	436 FVCKVEHTELASMKEVFLFKEKGEYNTPSVYVFPPPLEELSKRETATLTCLVKGFSPSEI 495		377 LVSNMANSEDLRSISWFKKSGTQEIPLKTELGDAIYNDNRTYSVKGTTTVCADEWNNDK- 435		441 VVVDVSHEDDEVKEVMY-VDGVEVHAKTKEREFOYNSTVRVVSVT.TVT.HODWI.NGKE 497	336 EKNMSKSEMCDIFIIETSI		381 ESNIKVLPTWSTPVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC 440	280 ENNGNOTTEGVKVEEFVEUKKKGTEATSTESTIKKEMULUTLISCVVEHAESGS-LQ 335		PVWVLNPEA	rvat	cal Similarity 29.5%; Pred. No. 8.7e-17;	Match 9.8%; Score 333.5;	SEQUENCE 587 AA; 64933 MW; 646B5FD0FA414E8D CRC64;	Hypothetical protein.	to the	Klein S., Strausberg R.;	SEQUENCE FROM N.A. TISSUE=Spleen;

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29027 Q29027 Q29027 Q29027 Q29027 Q29027 Q29027 Q29027 Q2902 Q2902
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=#1183; TISSUE=Blood;
STRAIN=#23329116; PubMed=8335933;
MEDLINE=93329116; PubMed=8335933;
Gustafsson K., Germana S., Sundt T.M.
Gustafsson Kanada S., Sundt T.M.
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01-NOV-1996 (TrEMBLrel. 01, C
01-NOV-1996 (TrEMBLrel. 01, L
01-CCT-2003 (TrEMBLrel. 25, L
CD4, allel 1 (Fragment).
Sus scrofa (Pig).
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                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HPPSQSTVKRVIRNQKVDCRQTDI----SVSLLKP-PFEEIWTQQTATIVCEIV---YSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----WO----KDDVSVSANVTNFPTALEQDLTFSTRSLLNLTAVEWKSGAK-YTCTAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----QSGVEYTCSAKQDQSSTPVVKRTRKARVEPTKP-HLRLLPPSPEEIQSTS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLSTVSAG-----VVVSWMVNGKV--RNEGVQMEPTKMSGNQYLTISRLTSSVEEW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVE---FSFPLAFTVEKLTGSGELWWQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -SHSATSSNQRKEIRST----SEIAVLLRDP---
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                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
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                                                                     Sachs D.H.,
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Q7Z379;
01-OCT-2003
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bloecker H., Boecher M., Mewes H.W., Weil B., Fobo G., Han M., Wiemann S.; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ EMBL; BX538066; CAD97996.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein DKFZp686K04218 (Fragment).
DKFZP686K04218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Human rectum tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               132;
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59; Conserv
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                                                                   TAFDIWGQGTVVTVSSASPTSPKVFPLSLDSTPQDGNVVVACLVQGFFPQEPLSVTWSES
                            GM----
                                                                                                                LTCEVWG-----PTSPKLM-LSLKLENKEAKVSKR---
                                                                                                                                                                                                         HLTLPQALPQYAGS-----GNLTLALEAKTGKLHQEVN-----LVVMRATQLQKN
                                                                                                                                                                                                                                                         FSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPL
                                                                                                                                                                                                                                                                                                                                                    LSQVQLQESGPGLVKPSQTLSLTCTV------SGGSI-----SGGSI
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                                                                                                                                                              ----MGYIYYSGSTYYNPSLESRLSISIDTSKNQFSLRLNSLTAADTAVYFCARGVGLG
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llarity 60.2%;
Conservative 16
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                   -WQCLLSDSGQVLLESNIKVLPTWSTPVEPKS--CD-KTHTCP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               66;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 302.5; DB 4;
Pred. No. 1.5e-14;
6; Mismatches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 305.5; DB 6;
Pred. No. 9.3e-16;
.6; Mismatches 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 478;
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----EKPVWVLNPEA 365
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IN SEQUENCE FROM N.A.

IN TISSUE-Mammary gland;

IN A INSIGNATION OF T., OTE T., Augash K., Sugano S., Shiratori A., Sudo H.,

UA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

UA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

UA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

UA Watanabe S., Kimura K., Murakawa K., Ono Y., Takiguchi S.,

UA Watanabe S., Kimura K., Murakawa K., Ishi S., Kawai Y., Saito K.,

UA Watanabe S., Kimura K., Murakawa K., Ishi S., Kawai Y., Saito K.,

UA Watanabe S., Kimura K., Murakawa K., Ono Y., Takiguchi S.,

UA Watanabe S., Kimura K., Murakawa K., Ono Y., Takiguchi S.,

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UA Watanabe S., Kimura K., Murakawa K., Ono Y., Takiguchi S.,

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UA Watanabe S., Kimura K., Murakawa K., Ono Y., Takiguchi S.,

UA Watanabe S., Kimura K., Murakawa K., Ono Y., Takiguchi S.,

UA Watanabe S., Kimura K., Murakawa T., Noo Y., Takiguchi S.,

UA Watanabe S., Kimura K., Murakawa T., Noo Y., Takiguchi S.,

UA Watanabe S., Kimura K., Murakawa T., Noo Y., Takiguchi S.,

UA Watanabe S., Kimura K., Murakawa T., Noo Y., Takiguchi S.,

UA Watanabe S., Kimura K., Murakawa T., Noo Y., Takiguchi S.,

UA Watanabe S., Kimura K., Murakawa T., Noo Y., Takiguchi S.,

UA Watanabe S., Kimura K., Murakawa T., Nakamura T., Nakamura T., Nakamura T., Nakawa T., Noo Y., Takiguchi S.,

UA Watanabe S., Kimura T., Nakamura T., Nakawa T., Nakamura T., N
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Best Local Similarity
Matches 140; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q96K68 PRELIMINARY; PRT; 494 AA.
Q96K6B;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ14473.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Bukaryota; Metazoa; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 494 AA; 53088 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                    NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG
                                                                                                                                                                                                                                                             LVKPGGSLRLSCAASGLSFSTYAMNWVRQAPGKGLEWVSSISSRSDYIYYRDSVKGRFTI
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                                                                                                                                                                                                                                                                                                                                      LGKKGDTVELTCTAS--QKKSIQFHW-----KNSNQIKILGNQGSFL----TKGPSKL
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                                                                                                                                                                                                                                                                                                                                                                                                       8.7%;
llarity 21.9%;
Conservative 85
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                                                                                                                                                                                                                                                                                                                                                                                                           85;
                                                                                                                                                                                                                                                                                                                                                                                                       Score 298.5; DB 4;
Pred. No. 3.1e-14;
5; Mismatches 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9A1D7AEB5AEE4C0E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                    136
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                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 57
1096KX8
10 Q96KX
AC Q96KX
DT 01-D1
DT 01-D1
DT 01-D2
DT 01-D2
DT 01-D3
DT 01-D3
DT 01-D4
DT 01-D5
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                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 133
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Q96KX8;
O1-DEC-2001 (TrEMBLrel. 19, C
01-DEC-2001 (TrEMBLrel. 19, I
01-OCT-2003 (TrEMBLrel. 25, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Lung;
                                                                                                                                                                                                                                                     Local Similarity
nes 133; Conserv
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A Strausberg R.;
Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC016369; AAH16369.1; -.
R InterPro; IPR007110; Ig-1ike.
InterPro; IPR003006; Ig_MC.
R InterPro; IPR003596; Ig_v.
R Pfam; PF00047; ig; 4.
R Pfam; PF00047; ig; 4.
R SMART; SM00406; IGv; 1.
R PROSITE; PS05035; IG_LIKE; 4.
R PROSITE; PS05099; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
LVVMRATQ--LQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCL 371
                                                                                                                          GLTANSDTHLLQGQSLTLTLESPPGSSPSVQ----CRSPRGKNIQGGKTLSVSQL-----E
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                                                                          GLVKSSET-----LSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIANTYYSGITYYNPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FYPSDIAVEWESNGO -- PENNYKTTPPVLD-SDG--SFFLYSKLTVDKSRWQQGNVFSCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----SPSTPPTP----SPSTPPTPSPSCC-HPRLSLHRPALED-LL
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                                                                                                                                                               8.7%; bu-
23.5%; Pred
4ve 72;
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Last annotation updat
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                                                                                                                                                                         Score 296; DB 4; 1
Pred. No. 4.9e-14;
2; Mismatches 205;
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                                                               Query Match
Best Local S
Matches 133
                                                                                                                                                                                  InterPro; IPR003599; Ig.
InterPro; IPR00710; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00306; Ig_V.
Pfam; PF00047; Ig; 4.
SMART; SM00409; IGc1; 2.
SMART; SM00407; IGC1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QBN5K4; PRELIMINARY;
QBN5K4;
01-OCT-2002 (TrEMBLrel. 2
01-OCT-2002 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2
                                                                                                                                                 Hypothetical
SEQUENCE 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-2002) to the EMBL; BC032249; AAH32249.1; InterPro; IPR003599; Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWES
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499 AA; 5
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25.8*;
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                                                                  61;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ
                                                               Score 295; DB 4; Length Pred. No. 5.9e-14; 1; Mismatches 202; Indel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; I
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                   93A5C89582054F32 CRC64;
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  Query Match
                                                                          InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 4.
SMART; SM00409; IG; 4.
SMART; SM00407; IGC1; 2.
SMART; SM00407; IGC1; 2.
SMART; SM00405; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8NCL6
Q8NCL6;
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Mammary gland;
Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T.,
Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y.,
Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagah
Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
Hypothetical protein FLJ90170.

Bukaryota, Metazoa; Chordata; Craniata; Vertebrat
Mammalia; Eutheria; Primates; Catarrhini; Hominid
                                         Hypothetical SEQUENCE 4
                                                                                                                                                                                                                                                                                                                    Hattori A., Okumura K., Iwayanagi T., Ninomiya K.; "NEDO human cDNA sequencing project."; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AK074651; BAC11114.1; -.
                                                                                                                                                                                                                                                      InterPro; IPR003599;
InterPro; IPR007110;
InterPro; IPR003597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSDIAVEWESNGQ--PENNYKTTPPVLD-SDG--SFFLYSKLTVDKSRWQQGNVFSCSVM
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                                            1 protein.
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                                         53224 MW; 12ECD7E094777101 CRC64;
                                                                                                                                                                                                        Ig.
Ig-like.
Ig_cl.
Ig_MHC.
Ig_v.
  8.6%;
  Score 292;
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  Length 493;
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., Saito K.,
yahari K.,
Sasaki N.,
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Q9NPF AC Q9NPF AC Q9NPF AC Q9NPF D1 01-00 D1-00 D1-00 D1-00 D2 Immun OS Homo OC Eukar OX NCBI RN [1] - RN [1] - RN [2] RP SEQUE RA PLVI RL Submi RL Submi RA Lehra RT Juhe RA Lehra RT Submi DR HSSP;
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Matches
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SEQUENCE FROM N.A.
Pluvinet R., Estivill X.,
Pluvinet R., 2000) to t
                                                                                                                                                                                                                             Q9NPP6;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
Immunoglobulin heavy chain )
human gene transcripts.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL389978; CAB97534.1; -.
HSSP; P01789; 1MCP.
                                                                                                                                                                                       Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria; E
                                                                                                                                                                                                                                                                                                   Q9NPP6
                                              Auffray C., Ansorge W., Ballabi
Lehrach H., Poustka A., Lundebe
"The European IMAGE consortium
                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                             EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNKVVLGKKGDTVELTCTAS--QKKSIQFHWKNSNQ-----IKILGNQG-----SFLTK
                                                                                                                                                                                                                                                                                                                                                                     TFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTC
                                                                                                                                                                                                                                                                                                                                                                                                                           CLARGESPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRVAAEDWKKGD
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                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                        Chordata;
Primates;
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                                              Ballabio A., ;
, Lundeberg J.;
nsortium for in
                                                                                                                       the
                                                                                                                    Escarceller M., Sumone EMBL/GenBank/DDBJ
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0; Mismatches 203;
                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                    PRT;
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                                                                              Estivill X.,
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InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
SMOSITE; PS50835; IG_LIKE; 3
PROSITE; PS00290; IG_MHC; 2.
                                           InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50830; IG_MHC; 1.
                                                                                                                                                                                                                                                                           Q9BRV0;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2003 (TrEMBLrel. 25,
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PROSITE;
NON_TER
                                                                                                                                                                                                                                                    Hypothetical protein. Homo sapiens (Human).
                       Hypothetical
SEQUENCE 50
                                                                                                                                Submitted (APR-2001) to the EMBL; BC005951; AAH05951.1; HSSP; P01789; 1MCP.
                                                                                                                                                                   Strausberg R.;
                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                             Q9BRV0
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                                                                                                                                                                               TISSUE=Prostate;
                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PREPOVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      K--SAVQGPPERDLCGCYSVSSVLPGCAQPWNHGETFTCTAAHPELKTPLTANITKS-GN
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                                                                                                                                                                                                                                                                                                                                                                                                                -LQLDETC 632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               -SDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG-----
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
                       al protein.
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                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                           415
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28.0%;
                                                                                                                                                                                                                               Chordata;
Primates;
                       54154 MW;
 8.48;
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                                                                                                                                                                                                                                                                            Last sequence update)
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Pred. No. 9
 Score
                                                                                                                                                                                                                               Craniata; Vertebrata;
Catarrhini; Hominidae
                       0A9BF43F2A3CC6D9 CRC64;
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 288;
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 4.
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Length
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                                                                                                                                                                                                                                          Euteleostomi;
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              TISUE-Gastric micosa;

TISUE-Gastric micosa;

A Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Albuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J., Albuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J., Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kaw Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugi Sugiyama T., Nagai K., Isogai T., Sugano S.;

T. Nagai K., Isogai T., Sugano S.;

T. NEDO human cDNA sequencing project.";

Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AKOS8027; BAB71633.1; -

InterPro; IPR007110; Ig-like.

InterPro; IPR003596; Ig_MHC.

InterPro; IPR003596; Ig_MHC.
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Q96DK0;
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                           Hypothetical protein FLJ25298.
Homo sapiens (Human).
Eukaryota, Metazoa; (hordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG--SFFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DRDLCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKS-GNTFRPEVHLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTLALEAKTGKLHQEV------NLVVMRATQLQKNLTC-----EVWG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILFLVAAATGAQSQVHLVQSGAEVMS----PGASVRVSCKT-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VQLLVFGLT-ANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLEL
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8; Mismatches
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                                                                                                                 ., ono J., chiba d., Chiba M., Yamashita H., Chiba ., Morinaga M., Kawamura M. Nishikawa T., Sugivam
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                                                                                                                                                                   Chiba Y.
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TISSUE=Human rectum tumor;
Bloecker H., Boecher M., Mewes H
Fobo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL,
EMBL; EX538077; CAD98001.1; -.
Hypothetical protein.
NON TER

EMBL/GenBank/DDBJ

databases Amid

H.W.,

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Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;

Catarrhini; Hominidae;

Homo

Craniata; Vertebrata; Euteleostomi;

SEQUENCE

FROM N.A.

Homo sapiens (Human)

SEQUENCE

492 AA;

53776

WW.

1E7A15760F0CA74B CRC64;

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RESULT
Q7Z374
SO SERVICE 
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Best Local
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Q7Z374;
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
Hypothetical protein DKFZp686CO2218 (Fragment).
DKFZP686CO2218.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFT-VEKLTGSGELWWQAERAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQVHLVQSGAELKM----PGSSVKVSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTC
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A Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; BC013539; AAH13539.1; -.

R MGD; MG1:96486; Igh-VJ558.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR003006; Ig_MHC.

R InterPro; IPR003596; Ig_V.

R Pfam; PP00047; ig; 4.

R PROSITE; PS00359; IGV; 1.

R PROSITE; PS00359; IG MHC; 2.

M Hypothetical protein.

SEQUENCE 488 AA; 52964 MW; F12068460B400B9D CRC64;
                                                                                                                                                           Query Match
Best Local Similarity
Matches 126; Conserv
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Matches 102; Conserv
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01-DEC-2001 (TrEMBLrel. 19, Last
01-DEC-2001 (TrEMBLrel. 25, Last
01-OCT-2003 (TrEMBLrel. 25, Last
Hypothetical protein.
IGH-VJ558 OR A1893585.
Mus musculus (Mouse)
Eukaryots Metazoa; Chordata; Cr
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                                                                                                   PGSSPSVQCRSPRGKNI------QGGKTLS-VSQLELQDSGTWTCTVLQNQKKVEF
                                                    PGASVKLSCKA-SGYTITDYYVNWVKQSHGKSLEWIGDINPYNGGT-----SYNQK---F
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                                                                                                                                                        8.3%; Score 282; DB 11;
24.5%; Pred. No. 5.6e-13;
tive 78; Mismatches 198;
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27.9%; Pred. No. 2.8e-13;
:ive 47; Mismatches 137;
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Last annotation update)
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Best Local
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. Cao W., Cai X., Geng Zheng S., Cao J., Cao W., Cai X., Geng Indentification and characterization of regulated in colorectal cancer."; Submitted (JUN-1998) to the EMBL/GenBar EMBL; AROF07420; AAC19365.1; -. HSSP, P01825; JPAB
                                                                                                                                        Pfam; PF00047; ig; 3.
SMART; SM00407; IGc1; 2.
SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        O9UP60 PRELIMINARY;
O9UP60;
O1-MAY-2000 (TrEMBLrel. 13,
O1-MAY-2000 (TrEMBLrel. 13,
O1-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                           SNC73 protein.
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
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       363
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                                  91
                                                                                                    h 8.2%;
Similarity 26.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       K-GKATLTVDKSSIAYMQ------LINULTSDDSAVYYCARGPVYYSYFSYD
       PEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVEPKSCDKTHTCPPCPAPELLGGPSVFLF 422
                                                           TGKLHQEVNLVVMRATQ--LQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FPPKPKDTLMISRTPEVTCVVVDVSHEDPE-VKFNWYVDGVEVHNAKTKPREEQYNST--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CPEGESVKCSVQHDSNPVQELNVNCPGICSPP-----TTPPPPSCQ----PSLSL
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                                  SGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QRPALED-LLLGSDASITCTLNGL--RDPEGAVFTW-----EPSTGKDAVQKKAVQNSCG
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                                                                                        Conservative
                                                                                        49;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                     Score 281.5; DB 4; Pred. No. 4.3e-13;
                                                                                                                                               BA7ADC3CA5A9DD48 CRC64;
                                                                                       Mismatches 132;
                                                                                                                                                                                                                                                                                                               Geng L.;
ion of SNC73,
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132

CPVPSTPPTP----SPSTPPTPSPSCC-HPRLSLH

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Matches 55
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QBWY24;
QBWY24;
01-MAR-2002 (TrEMBLre
01-MCT-2003 (TrEMBLre
01-OCT-2003 (TrEMBLre
SNC66 protein.
Homo sapiens (Human).
Eukaryota; Metazoa; (
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=#1183, TISSUE-Blood, MEDLINE-93329116; PubMed-8335933; Gustaffson K., Germana S., Sundt T. "Extensive allelic polymorphion in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                          (TrEMBLrel. (TrEMBLrel. (TrEMBLrel. )
                                                                                                                                                                                                                                                    PRELIMINARY;
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          Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.2%; Score 280.5; DB 6; 56.1%; Pred. No. 7.5e-14; tive 19; Mismatches 23;
                                                                                                          20,
                                                                                                      Created)
Last seq
Last anno
          Craniata; Vertebrata;
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                                                                                                             sequence update) annotation updat
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          Euteleostomi;
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Sus.
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"Identification and characterization of SNC66, a Ig-like ge
down-regulated in colorectal cancer.";

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF283666; AAL36987.1; -.

R InterPro; IPR003106; Ig_MHC.

R InterPro; IPR003006; Ig_MHC.

R InterPro; IPR003596; Ig_W.

R Pfam; PF00047; ig; 4.

R PFASITE; PS50835; IG LIKE; 4.

R PROSITE; PS00290; IG_MHC; 1.

SEQUENCE 497 AA; 53665 MW; F24D08DFA5A663E5 CRC64;
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Best Local S
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448
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                                                                                    Q-VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG--SFFLYSKLTVDKS
                                                                                                                                                 VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN
                                                                                                                                                                                                                                                                                                   VIACLVQGFFPQEP---LSVTWSESGQGVTARNFP----PSQDASGDLYTTSSQLTLPA
                                                                                                                                                                                                                                                                                                                                                                                            LPQALPQYAGSGNL---
DWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTC
                            RWOOGNVFSCSVMHEALHNHYTOKSLSLSPG---
                                                           ELVTLTCLARGESPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRVAAE
                                                                                                                       VSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLPKS
                                                                                                                                                                                 LHRPALED-LLLGSEANLTCTLTGL-RDASGVTFTWTPSSGK--SAVQGPPERDLCGCYS
                                                                                                                                                                                                             LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
                                                                                                                                                                                                                                         TQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTP----SPSTPPTPSPSCC-HPRLS
                                                                                                                                                                                                                                                                       -----NIK------VLPTWSTPVEPKSCDKTHTCPPCPAPELLGGPSVF
                                                                                                                                                                                                                                                                                                                                                               TEDSAIYFCARGNLRGGRGFGYNWFDPWGHGTLVTVSSASPTNPKVFPLSLCSTQPDGNV
                                                                                                                                                                                                                                                                                                                                                                                                                         VRQAPGQGLEW-----MGWMNPQTGNTEFAQKFQGRLTFSRDTSINTAYMVLSSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      VEKLTGSGELWWQAERASSSKSWITFDLKNKEVSVK---RVT--QDPKLQMGKKLPLHLT
                                                                                                                                                                                                                                                                                                                               -LTCEVWG--PTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 279.5; DB 4;
Pred. No. 8.9e-13;
2; Mismatches 196;
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                                                                                                                     -GNTFRPEVHLLPPPSEELALN
                             ---LQLDETC
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Ig-like
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Submitted (
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01-JUN-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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     tted (MAR-2003) to the BC049143; AAH49143.1;
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                                                                                                                                                                                                                                                                                                                                                    Chordata;
Rodentia;
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25,
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Last annotation updat
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                                              EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Best Local Similarity
Matches 129; Conserv
                                                             099KA4 PRELIMINARY;
099KA4;
01-JUN-2001 (TrEMBLrel. 17, C
01-JUN-2001 (TrEMBLrel. 25, L
01-OCT-2003 (TrEMBLrel. 25, L
Hypothetical protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia, Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003596; Ig_w.
Pfam; PF00047; Ig; 3.
SMART; SM00409; IG; 3.
SMART; SM00409; IGc1; 3.
SMART; SM00406; IGv; 1.
PROSITE; PS00290; IG_MHC; 2.
Hypothetical protein.
SEQUENCE 487 AA; 53019 MW;
SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                 461
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                                                                                                                                                                                                                                                                                                                                                                                                              KTIDRLSG
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Rodentia;
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                                                                                                                                                                            Last sequence update)
                                                                                                                                                                                                                               Created)
                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Best Local S
Matches 142
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein. SEQUENCE 487 AA; 5
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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ
EMBL; BC004786; AAH04786.1; -.
HSSP; P01810; 2FBJ.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                  CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----KNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MNRGVPFRHLLLVL---QLALLPAATQGNKVVLGKKGDTVELTCTAS--QKKSIQFHW--
PGEGATTYLVTSVLRVSAETWKQGDQYSCMVGHEALPMNFTQKTIDRLSG
             DSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                 TFPPQVHLLPPPSBELALNELVSLTCLVRAFNPKEVLVRWLHGNEELSPESYLVFEPLKE
                                                             PREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ----PENNYKTTPPVL
                                                                                               TGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPESDT-LTGTIAKITVN
                                                                                                                NAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
                                                                                                                                                                                              PQ---YAGSGNLTL-ALEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKL
                                                                                                                                                                                                                                                                                                                                                                                                           ----ARDMGGSPYGGYSRFD---YWGQGTTITVSSESARNPTIYPLTLPRA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                             QTPEKRLEWVATISDGGSY-TYYPDNVKGRFTISRDN-AKNNLYLQMSHLKSEDTAMYYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MNFGLSLIFLVLVLKGVQCEVQLVESGGGLV---KPGGSLKLSCAASGFTFSSYAMSWVR
                                                                                                                                                                                                                             ENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVEPKSCDKTHT
                                                                                                                                                                                                                                                         ASGGGYTMSSQLTLPAVEC------
                                                                                                                                                                                                                                                                                                                                 VEKLTGSGELWWQAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQAL
                                                                                                                                                                                                                                                                                                                                                                                    LSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                   EVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSV-QCRSPRGKNIQGGKT
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21.8%;
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                                                                                                                                                                                                                                                                                                                                                          -----LSSDPVII-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 274.5; DB 11;
Pred. No. 2.1e-12;
1; Mismatches 220;
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                                                                                                                                                                                                       -SGPPPP-----
                                                                                                                                                                                                                                                                                                          -----VNFPPAL
                                                                                                                                                                                                                                                                                                                                                            -GCLIHDYFP----
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 468
                         625
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                                                                                                                                                                                                                                                                                                            200
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RESULT 70

O88650

ID O88650

AC O88650;

PRELIMINARY;

PRT; 120 AA.

AC O88650;

DT 01-NOV-1998 (TrEMBLrel. 08, Created)

DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE T-cell surface glycoprotein CD4 (Fragment).

GN CD4.

GN CD4.

Marmota monax (Woodchuck).

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                                                                 Query Match
Best Local S
Matches 135
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Best Local
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUE-Peripheral blood;
MEDLINE-20094937; PubMed=10627561;
MEDLINE-20094937; PubMed=10627561;
Guo J.T., Zhou H., Liu C., Aldrich C., Saput
Guo J.T., Zhou H., Liu C., Aldrich C., Saput
Guo J.T., Alon W.S., Seeger C.;
The second of the paraccytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8VCX4;
Q8VCX4;
01-MAR-2002
01-MAR-2002
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NON_TER
SEQUENCE
                                                                                                                                                                                        Pfam; PF00047; 19; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein. IGH-VJ558 OR AI893585.
                                                                                                                                                       Hypothetical
SEQUENCE 40
                                                                                                                                                                                                                                                                              InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                  Submitted (DEC-2001) to the EMBL; BC018322; AAH18322.1; MGD; MGI:96486; Igh-VJ558.
                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Apoptosis and regeneration of hepat
transient hepadnavirus infections.";
J. Virol. 74:1495-1505(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0016020; C:membrane; IEA.
GO; GO:0016955; P:lmmune response;
InterPro; IPR000973; CD4 TCA9.
InterPro; IPR007110; Ig-Tike.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
                                                                   Local Similarity
nes 135; Conserv
118 VQLLVFGLTA--NSDTHLLQ-GQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            308 LHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGM 367
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120 AA;
                                                                                                                                                       489 AA;
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                                                                   Conservative
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Rodentia;
                                                                                                                                                       53208 MW;
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25,
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Last annotation update)
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8; Mismatches
                                                               Score 272.5; DB 11;
Pred. No. 3e-12;
7; Mismatches 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 273; DB 11;
Pred. No. 3.7e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44967B512D520195
                                                                                                                                                       CC85B1194DAFEF2C CRC64;
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                                                                 Indels 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                         Length
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                                                                                                            489;
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RESULT 72
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                                                   Matches
                                                              Query Match
Best Local (
                                                                                                                                                                                                                                                                                                  T-cell surface glycoprotein CD4 precursor.
Anas platyrhynchos (Domestic duck).
Anas platyrhynchos (Domestic duck).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
                                                                                                                                                                                                                                                                                                                                Q90WB5;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
                                                                                                                    Signal.
SIGNAL
                                                                                                                                                                                                                      Chan S.W.S., Middleton D.L., Submitted (MAY-2001) to the
                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                   TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                            Q90WB5
                                                                                                                                                          Pfam; PF00047; ig; 4
SMART; SM00409; IG; :
                                                                                                                                                                                                           EMBL; AF378701; AAK59279.1; -.
                                                                                                                                                                                                                                                                                      NCBI_TaxID=8839;
                                                                                                                                            PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                 InterPro; IPR003599; InterPro; IPR007110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            460
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                                                   111;
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                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HWIKORSGOGLEWIGWFNPGSGSIKFNEK---FK-DKATLTADKSSTTVY---
RAVFVLLQLGL--THIMAHQQQIGVEGKEVILNC---KKHDKDVTWKYEYDAGSSAIIIQ
                        RHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWK-----NSNQIK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FTQKTIDRLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YTOKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WLHGNEELSPESYLVFEPLKEPGEGATTYLVTSVLRVSAEIWKQGDQYSCMVGHEALPMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WESNGQ---PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVTHPESDT-LTGTIAKVTVNTFPPQVHLLPPPSEELALNELVSLTCLVRAFNPKEVLVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L--RDPEGAVETW----
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                                                                                                      482 AA;
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                            8.0%;
25.0%;
                                                                                                      54624 MW;
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                                                                                                                    29
                                                                                                                                                                                Ig.
Ig-like.
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                                                   69;
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                                                                                                                                                                                                                         Lundqvist M., Warr G.W., Higgins EMBL/GenBank/DDBJ databases.
                                                  Pred. No. 3.5e
); Mismatches
                                                                Score 271.5;
Pred. No. 3.9
                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                      BDA0E8EC6172AD0B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                             482
                                                                .5e-12;
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                                                                            DB 13;
                                                   169;
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                                                   Indels
                                                                           Length
                                                                                                                                                                                                                                                                                                                   Euteleostomi;
                                                   95;
                                                                                                                                                                                                                                     D.A.;
                                                  Gaps
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                                                                                                                                                 Query Match
Best Local Similarity
Matches 144; Conser
                                                                                                                                                                                                                          InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q99LA6
Q99LA6;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia, Eutheria; Rodentia;
                                                                                                                                                                                                    Hypothetical protein. SEQUENCE 484 AA; 5
                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (FEB-2001) to the EM
EMBL; BC003495; AAH03495.1; -.
PIR; F33932; F33932.
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                         HSSP; P01810; 2FBJ
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                 118
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                                                                                             4
VQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQ 177 : ; ; | | :17
                                         LKWMGWVNIETGESVYADDFKGRFAFSLETSASTIHLQINNLKNEDTATYFCARSDYDYD
                                                                                                                  VLQLALLPAATQGNKV------VLGKKGDTVELTCTASQKKSIQF--HWKNSNQIKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCHLMEDNNMKLSLNYTVEEAPTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLSWHLNF---RKIGWKEFFTGQLNWQEGNA-----TTYELLDFNATADGELRETK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HVKLTISSNGYFLPGDDLELTVMHKSPKSQPRFSITLFNSHNSRVTPEVLQNETPQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVFGLTANSDTHLLQGQSLTLT-LESPPGSSPS------VQCRSPRGKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFFLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QCLLSDSGQVLLESN--IKVLPTW 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILAGK---IFKGRAPMSDRSET----NONSKHLKVSNLRISDAGTYICECGSDRNSISL
                                                                   LGNOGSF-LTKGPSKLNDRADSRRSL---WDQGNFPLIIKNLKIEDSDTYICEVEDQKEE
                                                                                             VWTLLFLMAAAQSIQAQIQLVQSGPELKKPGETVKISCKASGYTFTDYSMHWVKQAPGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----LQKNLTCEVWGPTSPKLML-----SLKLENKEAKVSKREKPVWVLNPEAGMW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKKLPLHLTLPQALP------QYAGSGNLTLALEAKTGKLHQEVNLVVMRATQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EFSFPLAFTVEKLTG-----SGELWWQAERASSSKSWITFDLKNKEVSVKRVTQDPKLQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---KYALKVKQLQPTDSGTWICNMHSDSPSINENISFNVKVLGFEKTHLERMYAAVDSTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGPLPKGAEMTLLCQVSSPIPPNVHLLWERVNGTKMDGKKSKQS--ETKVEVKVTAVGMW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -KRSQALLEIPEMKRDSTVEVKIHKIQLKHSGEYTCQLLYNRRYIQSKTELVVMQVSANP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKI--DIVVLAFQKAS-SIVYKKEGEQV
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(TremBLrel. 17, Last seq
(TremBLrel. 25, Last ann
                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                 52567 MW; BEAEA4F9BCF582FA CRC64;
                                                                                                                                              8.0%; Score 271.5; DB 11; 22.6%; Pred. No. 3.5e-12; ive 76; Mismatches 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                               201;
                                                                                                                                               Gaps
                                         123
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Q91207
ID Q9120
AC Q9120
DT 01-DE
DT 01-DE
DT 01-DE
DT 01-DE
DT 01-DE
DT Mypot
OS Mus m
OC Eukaz
OC Mamma
OX NCEI-
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RN [1]
RN [1]
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DR FAM;
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                                                                                                                                 Query Match
Best Local S
Matches 98
                                                                                                                                                                                             A Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL, BC010324; AAH10324.1; -.

R InterPro; IPR0070110; Ig-11ke.

R InterPro; IPR003006; Ig_WHC.

R InterPro; IPR003596; Ig_v.

R Pfam; PF00047; ig; 4.

R SMART; SM00406; IGv; 1.

R PROSITE; PS50835; IG LIKE; 4.

R PROSITE; PS00290; IG_MHC; 2.

W Hypochetical protein.

Q SEQUENCE 486 AA; 52682 MW; 4FEF835125DA870B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q91Z07; PRELIMINARY;
Q91Z07; O1-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368
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                               331 WGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTW
                                                                                              282 LTLPQALP------QYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQKNLTCEV 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124
                                                                                                                               h 7.9%; Score 270.5; DB 11; Length 486;
Similarity 26.9%; Pred. No. 4.2e-12;
98; Conservative 54; Mismatches 143; Indels 69;
 TLPA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ---PENNYKTTPPVLDSDG--SFFLYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEELALNELLSLTCLVRAFNPKEVLVRWLHGNEELSPESYLVFEPLKEPGEGATTYLVTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NSCGCYSVSSVLPGCAERWNSGASFKCTVTHPE-SGTLTGTIAKVTVNTFPPQVHLLPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSLSLQRPALED-LLLGSDASITCTLNGLRNPEGAV-FTW----EPSTGKDAVQKKAVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLPAVECPEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LWWQAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IYAM------DYWGQGTSVTVSSES-----ARNP-----TIYPLTLP
                                                                LTLPRALSSDPVIIGCLIHDYFPSGTMNVTW-GKSGKDITTVNFPPALASGGGYTMSSQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLRVSAETWKQGDQYSCMVGHEALPMNFTQKTIDRLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVQELD-----TIPSCQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TL-ALEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VTW----GKSGK------YTMSSQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSGTWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              486
VECPEGESVKCSVQHDSNAVQELDVKC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -ESVKCSVQHDSN
                                                                                                                                   69;
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RESULT 75

Q91WT1

ID Q91WT1

AC Q91WT1

DT 01-DEC-2001

DT 01-DEC-2001

DT 01-OCT-2003

DE Hypothetical

OS Mus musculus

OC Eukaryota; Mu

OC Mammalla; Eu

OC NCBI_TAXID=10

RN [1]

RN [1]

RN [1]

RR SEQUENCE PRO

RC TISSUB=Colon

RA Scrausberg RC

RI Submitted (SI

DR InterPro; IPP

DR SMART; SM0044

DR SMART; SM0044

DR PROSITE; PS00

KW Hypothetical

SQ SEQUENCE 44
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_MHC; 2.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                      Hypothetical 
SEQUENCE 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC013490; AAH13490.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SSUE=Colon;
                                                           144
                                                                                        184
                                                                                                                      116
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                            244
                                                                                                                                                     124
                                                                                                                                                                                                                                                                                                          139;
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                                                                                                                                                                                                                                                                            15
                                                                                                                                                   GLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSPESYLVFEPLKEPGEGATTYLVTSVLRVSAETWKQGDQYSCMVGHEALPMNFTQKTID 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVKFNWYVDGVEVHNAKTKPREEQYNST----YRVVSVLTVLHQDWLNGKEYKCKVSNKAL
                            RASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTL-ALE 302
                                                                                        CTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAE 243
                                                                                                                                                                                  IYPGDGNTKYNEKFKGKTTLTADKSSSTAYMFLSSLTSEDSAVYFC----
                                                                                                                                                                                                   SFLTKGPSKLNDRADSRRSLW---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVF
: | : | | | | |
                                                                                                                                                                                                                                            QVQLLQSGPB-----LVKPGASVKISCKASGYTFTSYYIHW-----VKQRPGQGLVWIGW
                                                                                                                                                                                                                                                                          QLALLPAATQGNKVVLGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKILGNQG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AV-FTW----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGPPPP-----
                                                                                                                      -TRGGGWAFDYWGQGTTLTVSSEPAREPT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DT-LTGTTAKITVNTFPPQVHLLPPPSEELALNELVSLTCLVRAFNPKEVLVRWLHGNEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STPVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP
-GKSGK---
                                                                                                                                                                                                                                                                                                                                                                      481 AA; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence up
(TrEMBLrel. 25, Last annotation
                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       625
                                                                                                                                                                                                                                                                                                                                                                      52105 MW;
                                                                                                                                                                                                                                                                                                                       7.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -CPPCP-PSC--HPSLSLQRPALED-LLLGSDASLTCTLNGLRNPEG
                                                           --IYPLTFPQALSSDPVI1GCLIHDYFP-----
                                                                                                                                                                                                                                                                                                       $; Score 270; DB 11; Length 4$; Pred. No. 4.5e-12;69; Mismatches 213; Indels
-DITTVNFPPALASGGR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                       97DF68D159463F65 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                                      Length 481;
-YTMSSQLTLPAVE
                                                           -SGTMNVTW----
                                                                                                                                                                                                                                                                                                         212;
                                                                                                                                                                                                                                                                                                         Gaps
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Q8K172
ID Q8
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           Pfam; PF00047; ig; 4.

SMART; SM00407; IGc1; 3.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 2.

SEQUENCE 482 AA; 52121 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QBK172;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
Similar to expressed sequence AI893585.
Mus musculus (Mouse)
                                                                                                                                                                                  PIR;
PIR;
PIR;
PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
PIR; F
                                                                                                                                                                                                                                                            PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8K172
                                                                                                                                                   PIR; PH1153; PH1153. InterPro; IPR007110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Breast
                                                                                                        InterPro;
                                                                                                                     InterPro;
                                                                                                                                                                           BL; BC028249; AAH28249.1; -
R; F33932; F33932.
R; PH1105; PH1108.
R; PH1108; PH1108.
R; PH1114; PH1114.
R; PH1114; PH1118.
R; PH1125; PH1125.
R; PH1125; PH1125.
R; PH1126; PH1126.
R; PH1127; PH1128.
R; PH1128; PH1128.
R; PH1131; PH1131.
R; PH1131; PH1131.
R; PH1134; PH1134.
R; PH1139; PH1134.
R; PH1139; PH1139.
R; PH1139; PH1139.
R; PH1142; PH1142.
R; PH1142; PH1142.
R; PH1151; PH1151.
R; PH1151; PH1151.
R; PH1152; PH1151.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303
                                                                                                   ; IPR007110; Ig-like.
; IPR003597; Ig_c1.
; IPR003006; Ig_MHC.
; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEIWKQGDQYSCMVGHEALPMNFTQKTIDRLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KNQ-VSLTCLVKGFYPSDIAVEWESNGQ---PENNYKTTPPVLDSDG--SFFLYSKLTVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPALED-LLLGSDASITCTLNGL--RDPEGAVFTW----EPSTGKDAVQKKAVQNSCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LNELVSLTCLVRAFNPKEVLVRWLHGNEELSPESYLVFEPLKEPGEGATTYLVTSVLRVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YSVSSVLPGCAERWNSGASFKCTVTHPESDT-LTGTIAKVTVNTFPPQVHLLPPPSEELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPKPKDTLMISRTPEVTCVVVDVSHEDPE-VKFNWYVDGVEVHNAKTKPREEQYNST---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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              A06FF083E771D084 CRC64;
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RESULT OF FEMALE RAPER R
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Best Local S
Matches 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9DCD9 PRELIMINARY; PRT; 426 AA. Q9DCD9; (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-OCT-2001 (TrEMBLrel. 25, Last annotation update) Adult male kidney cDNA, RIKEN full-length enriche clone:0610041A01, full insert sequence.

Mus musculus (Mouse).
SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUB-Kidney;

MEDLINE-21085660; PubMed-11217851;

MEDLINE-21085660; PubMed-11217851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii

Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka

Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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0; Mismatches
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Pred. No. 4.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
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Best Local S
Matches 98
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InterPro; IPRUVU
Pfam; PP00047; ig; 4.
SMART; SM00407; IGcl; 2.
PROSITE; PS50835; IG_LIKE; 3.
PS00290; IG_MHC; 2.
PS00290; NA; 45819 MW; F
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Q91WT3;
Q91WT3;
Q91WT3;
O1_DEC_2001 (TrEMBLrel. 19, Cre
01_DEC_2001 (TrEMBLrel. 25, Las
01-OCT_2003 (TrEMBLrel. 25, Las
Hypothetical protein.
IGH-VJ558 OR AI893585.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Rodentia; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T. Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming I Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR;
                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Functional annotation of a full-length Nature 409:685-690(2001).
EMBL; AK002875; BAB22422.1; -.
  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P01810; 2FBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                             404
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  FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLPA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTLPRALSSDPVIIGCLIHDYFPSGTMNVTW-GKSGKDITTVNFPPALASGGGYTMSSQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DT-LTGTIAKITVNTFPPQVHLLPPPSEELALNELVSLTCLVRAFNPKEVLVRWLHGNEE
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IPR003597; Ig_cl.
IPR003006; Ig_MHC.
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Last
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Pred. No. 4.1e-12;
4; Mismatches 143;
                                                                           Craniata; Vertebrata;
Sciurognathi; Muridae;
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annotation updat
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; Murinae; Mus
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ID Q91X9
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AC Q91X9
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DT HYPOT
OS Mus m
OC Eukar
OC Mamma
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RN [1]
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RC TISSU
RA Straw
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Best Local Similarity
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Strausberg R;
Strausberg R;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ dai
EMBL; BCC13488; AAH13488.1; -.
MCD; MC1:96486; Igh-VJ558.
InterPro; IPR003106; Ig_MC.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 4.
PROSITE; PS00240; IG_LIKE; 4.
PROSITE; PS00259; IG_LIKE; 4.
PROSITE; PS00259; IG_LIKE; 4.
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Q91X92;
Q91X92;
Q91X92;
Q91X92;
Q91X92;
Q1-DEC-2001 (TrEMBLrel. 19
Q1-DEC-2003 (TrEMBLrel. 29
Hypochetical protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chorde
Mammalia; Eutheria; Rodent
  Strausberg
Submitted
                                                 SEQUENCE FROM N. TISSUE=Colon;
                                                                                                                  NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WTCTVL-----ONOKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLA---FT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VTSVLRVSAEIWKQGDQYSCMVGHEALPMNFTQKTIDRLSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --PSLSLQRPALED-LLLGSDASITCTLNGL--RDPEGAVFTW----EPSTGKDAVQKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE-VKFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKPVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVEPKSCDKTHTCPPCPAPELL 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTMNVTW-GKSGKDITTVNFPPALASGGRYTMSSQLTLPA---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNLTLALEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKR
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g R.;
(JUL-2001)
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                                                                                                                                               Chordata;
Rodentia;
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  EMBL/GenBank/DDBJ
                                                                                                                                                 Craniata; Vertebrata; E
Sciurognathi; Muridae;
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annotation update)
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                                                                                                                                                                         Euteleostomi;
                                                                                                                                                 Murinae;
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Best Local S
Matches 142
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SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 2.

Hypothetical protein.

SEQUENCE 482 AA; 51865 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; BC011181; AAH11181.1; 
PIR; F33932; F33932; 
InterPro; IPR007110; Ig-1ike 
InterPro; IPR003006; Ig_MHC. 
InterPro; IPR003596; Ig_v.
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142; Conserv
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                                                                                                                                                                                                                                NST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAMDYW------GQGTSVTVSSEPAREPT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQ
                                                                                                                                                                   SVLRVSAEIWKQGDQYSCMVGHEALPMNFTQKTIDRLSG
                                                                                                                                                                                         SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                 PSEELALNELVSLTCLVRAFNPKEVLVRWLHGNEELSPESYLVFEPLKEPGEGATTYLVT
                                                                                                                                                                                                                                                                QNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPESDT-LTGTTAKVTVNTFPPQVHLLPP
                                                                                                                                                                                                                                                                                                              PSLSLQRPALED-LLLGSDASITCTLNGL--RDPEGAVFTW-----EPSTGKDAVQKKAV
                                                                                                                                                                                                                                                                                                                                    PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE-VKFNWYVDGVEVHNAKTKPREEQY
                                                                                                                                                                                                                                                                                                                                                            PVQELNVNC
                                                                                                                                                                                                                                                                                                                                                                                   PVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                                                                                                                                                                                                                           TLPAVECPEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         VTW----GKSGK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LWWQAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DSGTWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLEWLGVIWTGGVTNYNSALKSRLSISKDNSKSQVFLKMNSLQTNDTARYYC-ARDSNYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ILGNQGSFLTKGPSKLNDRADSRRSL-WDQGNFPLIIKNLKIEDSDT--YICEVEDQKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LALLLCLVTFPSCAL-SQVQLKESGPDLVAPSQSLSITCTVSGFALTSYAISWVRQPPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                TL-ALEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 266; DB 11;
Pred. No. 9.1e-12;
1; Mismatches 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IYPLTFPQALSSDPVIIGCLIHDYFP
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                                                                                                                                                                   463
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Q91WP5 PRELIMINARY;
Q91WP5;
01-DEC-2001 (TrEMBLrel. 19, 0
01-DEC-2001 (TrEMBLrel. 19, 1
01-CCT-2003 (TrEMBLrel. 25, 1
Hypothetical protein.
Mus musculus (Mouse).

Created)
Last sequence update)
Last annotation updat

479

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Eukaryota; Metazoa; Mammalia; Eutheria;

Chordata; Rodentia;

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

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RESULT
Q8VEAO
ID Q8
AC Q8
AC Q8
AC O1
DT 01
DT 01
DT 01
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OC NO
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TISSUE=COLON;

TISSUE=COLON;

STRAUBBERG R.;

Submitted (SEP-2001) to the EMBL/GenBank/DDBJ dal
EMBL; BC013656; AAN113656.1; -.

InterPro; IPR003106; Ig_HC.

InterPro; IPR003006; Ig_MC.

InterPro; IPR003596; Ig_V.

Pfam; PF00047; Ig; 4.

SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS50835; IG_LIKE; 4.
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Best Local Similarity 24.7%;
Matches 134; Conservative 78
Q8VEA0

Q8VEA0;
Q8VEA0;
Q8VEA0;
Q1-MAR-2002 (TrEMBLrel. 20, Cres
Q1-MAR-2002 (TrEMBLrel. 25, Last
Q1-QCT-2003 (TrEMBLrel. 26, Last
Q1-QCT-2003 (TrEMBLrel. 20, Last
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GELWWQAERASSSKSWIT------FDLKNKEVSVKRVTQDPKLQMGKKLPLH-LTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----SW---VROSPEKRLEW-----VAAINSNGGNTYYSD-----TMKGRFTISRDNAK
                                                                                                                                                                                                                                                                                                                                                    SG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STLYLQ---MSSLRSEDTAFYYCVRGGYFDVWGAGTAV-TVSSEP----AREPTIYPLTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                               PESYLVFEPLKEPGEGATTYLVTSVLRVSAEIWKQGDQYSCMVGHEALPWNFTQKTIDRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PQALSSDPVIIGCLIHDYFPSGTMNVTW-GKSGKDITTVNFPPALASGGRYTMSSQLTLP
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Pred. No. 9.8e-12;
8; Mismatches 207;
  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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RESULT
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SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 2.

Hypothetical protein.

SEQUENCE 484 AA; 52859 MW;
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Mammalia; Eutheria; R
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Rodentia; Sciurognathi; Muridae; Murinae; Mus
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; Pred. No. 1.3e-11;
53; Mismatches 145;
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Best Local S
Matches 97
                                                       Query Match
Best Local Similarity
Matches 96; Conserva
                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC010798; AAH10798; 1; -.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O91XE1; PRELIMINARY; PRT; 480 AA.
091XE1; 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00407; IGc1; 3.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
SEQUENCE 488 AA; 53127 MW; 0E3B156E155733F0 CRC64;
                                                                                                                                                                                                                                                              Pfam; PF00047; 1g; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein (Fragment).

Mus musculus (Mouse).

Eukaryota, Metazoa; Chordara; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                              Hypothetical protein.
NON TER 1
SEQUENCE 480 AA; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atch 7.7%; Score 264; DB 11; Length 488; cal Similarity 26.6%; Pred. No. 1.3e-11; 97; Conservative 53; Mismatches 145; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           566
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   282 LTLPQALP------QYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQKNLTCEV 330
                                                             96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              405 ELSPESYLVFEPLKEPGEGATTYLVTSVLRVSAEIWKQGDQYSCMVGHEALPMNFTQKTI 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DRLSG 469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDT-LTGTIAKVTVNTFPPQVHLLPPPSEELALNELVSLTCLVRAFNPKEVLVRWLHGNE 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E-VKFNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKA 506
                                                                                                                                                                              480 AA; 51936 MW; 20B9234EEF2B41ED CRC64;
                                                                                     7.6%;
                                                       %; Score 261; DH 11;
%; Pred. No. 2.2e-11;
54; Mismatches 145;
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                                                                                                                 Length 480;
                                                          Indels
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85 PQALPQYAGSGNLTLALEAKTGKLHQEVNLVVWRATQLQKNLTCE	100 -MYLNNLTSEDSAFYYCAREWYG-AWFAFWGQGTLVTVSAESARNPTIYPLTL 150	ITFDLKNKEV	62 KSLEWIGYIDPYNGGSSYNQKFK-GKATLTVDKSSNTAF99	WTCTVLQNQKKVE	6 IFLELLSGTTGVHSEIQLQQSGPELVRPGTSVKVSCKASGYSFIDYNIYWVKQSHG 61	TLOG	Query Match 7.5%; Score 256.5; DB 11; Length 481; Best Local Similarity 22.9%; Pred. No. 4.8e-11; Matches 124; Conservative 82; Mismatches 215; Indels 121; Gaps 25;	Hypothetical protein. SEQUENCE 481 AA; 52326 MW; 52B44C5826807143 CRC64;	OSITE; PS5	ART; SM00406; IGV;	iterPro; IP	MBL; BC018455; AAH18455.1; nterPro; IPR007110; Ig-like.	bmitted (DEC-2001)	SEQUENCE FROM N.A. TISSUE=Breast tumor;	드胺	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Pornetical protein.	L-MAR-2002 (TrEMBLrel. 20, L-OCT-2003 (TrEMBLrel. 25,	-MAR-2002 (TrEMBLrel. 20, Created)	SOUCCUS PRELIMINARY; PRT; 481 AA.	T 84	457 DRLSG 461	621 SLSPG 625	397 ELSPESYLVFEPLKEPGEGATTYLVTSVLRVSAEIWKQGDQYSCMVGHEALPMNFTQKTI 456	NYKTT	338 SDT-LTGTIAKVTVNTFPPQVHLLPPPSEELALNELLSLTCLVRAFNPKEVLVRWLHGNE 396	507 LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ 565	283 EGAVFTWEPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPE 337	451 E-VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA 506	240 SPPTTPPPPSCQPSLSLQRPALED-LLLGSDASITCTLNGLRDP 282	:LLGG	205 TLPAVECPEGESVKCSVQHDSNPVQELNVNCPGIC 239	331 WGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTW 390	

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                                                                                                                                                                                                       RP SEQUENCE FROM N.A.

RC STRAIN=678L/6J; TISSUE=Breast tumor;

RX MEDLINE=22388257; PubMed=12477932;

RX MEDLINE=22388257; PubMed=12477932;

RX MEDLINE=2388257; PubMed=12477932;

RX Altausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Heine F.,

RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., McGernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Jones S.J., Marra M.A.,

RA Jones S.J., Marra M.A.,

RA Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q7TMK4;
01-OCT-2003
01-OCT-2003
Submitted (AUG-2003) to the EMEMBL; BC055905; AAH55905.1; -. Hypothetical protein.
SEQUENCE 479 AA; 52209 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q7TMK4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                    Strausberg R.;
Submitted (AUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                    STRAIN-C57BL/6J; TISSUE-Breast tumor,
                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                         Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85
                                                                                                                                                                mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -FTW-----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPE-SG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KFNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
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                                                                                                                                                              sequences."
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                                                    EMBL/GenBank/DDBJ databases
                                                                                                                                            99:16899-16903 (2002)
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Matches 110;
                                                        Matches
                                                                                                         Query Match
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                                                                                                                                                         InterPro; IPR003599; IG.
InterPro; IPR007110; IG-1ike.
InterPro; IPR003597; IG_c1.
InterPro; IPR003597; IG_c1.
InterPro; IPR003596; IG_w.
Pfam; PF00047; IG; 3.
SMART; SM00409; IG; 3.
SMART; SM00407; IGc1; 3.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00299; IG_MHC; 2.
SEQUENCE 480 AA; 51645 MW; 6
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QBKOZ1-
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QBKOZ1-
QBKOZ1-
QBKOZ1-
QBC (TEMBLrel. 22, Lass
Q1-OCT-2002 (TEMBLrel. 25, Lass
Q1-OCT-2003 (TEMBLrel. 25, Lass
Similar to expressed sequence A
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; BC029188; AAH29188.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                               Local
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  282 LTLPQALP------QYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQKNLTCEV 330
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                                                      1 Similarity
93; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YLVTSVLRVSAETWKQGDQYSCMVGHEALPMNFTQKTIDRLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ---PENNYKTTPPVLDSDG--S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
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                                                      Conservative
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                                                                            7.4%;
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Last annotation updat
ce AI893585.
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                                                   Score 251.5; DB 11;
Pred. No. 1.1e-10;
66; Mismatches 145;
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Pred. No. 1e-10;
                                                                                                                                                                  8690A63C669CDBED CRC64;
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InterPro; IPRO03006; Ig_MHC.
InterPro; IPRO03596; Ig_v.
Pfam; PF00047; 19; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIEE; 4.
PROSITE; PS50835; IG_MHC; 2.
Hypothetical protein.
SEQUENCE 479 AA; 51992 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            099M22;
099M22;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                     Submitted (JAN-2001) to the EMBL; BC002091; AAH02091.1; HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                               390 WSTPVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
                                                                                               331 WGPTSPKLMLSLKLENKEAKVSKREKPVWYLNPEAGMWQCLLSDSGQVLLESNIKVL-PT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               457
                                                                                                                                                                                        Similarity
                                                                                                                                                 LTLPQALP-----QYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQKNLTCEV 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNIKVL-PT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WSTPVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEVKFNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKA
                          PPPPI-----
                                                                                                                         LTLPPALSSDPVIIGCLIHDYFPSGTMNVTW-GKSGKDITTVNFPPALASGGRYTMSSQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -SGTLTGTIAKVTVNTFPPQVHLLPPPSEELALNELLSLTCLVRAFNPKEVLVRWLHGNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEVKFNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKA
                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -FTW----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     625
                                                                                                                                                                                                                           51992 MW;
                                                                                                                                                                                        25.5%;
                                                                                                                                                                                       7.3%; Score 250.5; DB 11; Length 25.5%; Pred. No. 1.4e-10;
                        -TIPSCO-----PSLSLQRPALED-LLLGSDASITCTLNGLRNPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -TIPSCQ-----PSLSLQRPALED-LLLGSDASITCTLNGLRNPE
                                                                                                                                                                           56;
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Last
                                                                                                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                           768E39A138918892 CRC64;
                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence update)
annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 479
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                                                                         VECPEGESVKCSVQHDSNPVQELDVNCSGPT
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                                                                                                                                                                           145;
                                                                                                                                                                           Indels
                                                                                                                                                                                                    479;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Mus
                                                                                                                                                                          Gaps
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506
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Best Local S
Matches 113
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01-NOV-1999
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goodchild M., Bumstead N., Vainio O.; "The chicken CD4 gene has remained conserved Immunogenetics 0:0-0(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=H.B2; TISSUE=Thymus;
MEDLINE=99218434; PubMed=10201936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD4 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9W6V7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9W6V7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ401223; CAC82027.1; -. InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; ig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=B12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koskinen R., Lamminmaki U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Koskinen R.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vainio O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning and modeling of the first nonmammalian CD4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunol.
                                              166
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183
                                                                                         126
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113; Conserv
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                                                                                                                                                                                                                               NOGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVF
                                                                                                                                                                                                                                                                               VILVLQLGLTPIMAQQEQQI-GIAGKEVILSCKAINNQKDGTCTWKYKYKEVSSTIISFS
                                                                                                                                                                                                                                                                                                                           LLLVLQLALLPAATQGNKVVLGKKGDTVELTCTA-SQKKSIQFHWKN-----SNQIKILG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DRLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAV-FTW-----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPE 336
---LKLKOLKAIDSGTWMCHVYSNSPSINONISFDVKVLGFEKERLEIIYTTVGNTAILS
                                           GKTLSVSQLELQDSGTWTCTVLQNQKKVEFKI--DIVVLAFQKAS-SIVYKKEGEQVEFS
                                                                                         KLTISSNGHFLTNEDLELTLMQNSSHSQPHLSIKLFNINNDIVTTEILQEEAPQ-KYI--
                                                                                                                                     GLTANSDTHLLQGQSLTLTL-ESPPGSSPS--
                                                                                                                                                                                      KAQVFKGKAPM-----THRSELNSNSKKLKVSDLSLDDAGIYTCACYSPVVSISLHVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.) (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      487 AA;
                                                                                                                                                                                                                                                                                                                                                                       7.0%;
ilarity 25.7%;
Conservative 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salomonsen J., Tregaskes Bumstead N., Vainio O.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IG_LIKE; 2
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12,
25,
                                                                                                                                                                                                                                                                                                                                                                       ; Score 240; DB 13;
; Pred. No. 8.8e-10;
61; Mismatches 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tregaskes
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
; B9CBA92EC9F7F45B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.A.,
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                                                                                                                                                                                                                                                                                                                                                                            184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                  -VQCRSPRGKNIQG
                                                                                                                                                                                                                                                                                                                                                                         82;
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DR RR P OCC OCC DTT DTC
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Q96RW7
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P70443
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Best Local S
Matches 45
                                                                                                                                                                                         Q96RW7;
Q96RW7;
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-OCT-2003 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P70443
P70443;
"Human hemicentin gene.";
Submitted (JUN-1999) to the
EMBL; AF156100; AAK68690.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BR/cdJ;
Rosenwasser O.A., Fairchild
Submitted (OCT-1996) to the
EMBL; U75219; AAB18133.1; -.
HSSP; P05540; ICID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mutant T-cell surface glycoprotein CD4 (Fragment).
                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                               Hemicentin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                             Homo sapiens (Human)
                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                       frent J.;
                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                      90
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                                                                                                                                                                                                                                                                                                                                                                                                                              QEVNLVVMKVAQLNNTLTCEVMGPTSPKWRLTLKQENQEARVSEEQKVVQVVAPETGLWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                               QEVNLVVMRATQLQKNLTCEVMGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQ
                                                                                                                                                                                                                                                                                                                                                                                             CLLSDSGQVLLESNIK 385
                                                                                                                                                                                                                                                                                                                                                             CLLSEGDKVKMDSRIQ 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNNKKISLNYTVEEAHVWNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRGGKMTLLCOVSGPLPSNAHLLWERVNGTQMEMKKSKQHEAKVEVNVSAPGLWNCHLVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----OKNLTCEVWGPTSPKLMLSLKLEN----KEAKVSKREKPVWVLNPEA-GMWQC-LLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIWFEISEGKTDGTMDVKIPKVOLNHSGQYKCQLEINGRRTESVRALVVMQVTAIPAGPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HL-----TLPQALP--QYAGSGNLTLALEAKTGKLHQEVNLVVMRATQL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WRLNFRKIKWKEGFTGKLNWEPQGNTAIHELLNFS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FPLAFTVEKLTG---SGELWWQAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSG-QVLLESNIKVLPTWST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90 AA; 9938 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                     PRELIMINARY;
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Rodentia;
                                                                                                                          Chordata;
Primates;
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19,
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                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
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EMBL/GenBank/DDBJ
                EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 237; DB 11;
Pred. No. 1.3e-10;
4; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6528B707928A4685 CRC64;
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                                                                                                                        Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                   5636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90
                                                                                                                      Vertebrata; Euteleostomi; ; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11;
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                databases
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Query Match
Best Local Sim.
Matches 154;
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Pfam; PF00090; tsp_1; 6.

SMART; SM001079; EGF CA; 7.

SMART; SM00108; IGCZ; 43.

SMART; SM00209; TSP1; 6.

SMART; SM00209; TSP1; 6.

SMART; SM00327; VWA; 1.

TIGREPAMS; TIGRO1451; B ant repeat; 9.

PROSITE; PS00100; ASX HYDROXYL; 5.

PROSITE; PS00108; GCROPIN; 1.

PROSITE; PS01186; EGF CA; 8.

PROSITE; PS01186; EGF CA; 8.

PROSITE; PS01187; EGF CA; 8.

PROSITE; PS00139; TIGLIFOTEASE_HIS; 1.

PROSITE; PS00639; TIGLIFOTEASE_HIS; 1.

PROSITE; PS00639; TSP1; 6.

EGF-like domain; Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
InterPro;
InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005727; C:extrachromosomal circular DNA; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000152; Asx_hydroxyl_S.
InterPro; IPR000152; Asx_hydroxyl_S.
InterPro; IPR000153; Gecropin.
InterPro; IPR001434; DUF11.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR005209; EGF_like.
InterPro; IPR00517; GFP_like.
InterPro; IPR007110; Ig-like.
InterPro; IPR00710; Ig-like.
InterPro; IPR003598; Ig_C2.
InterPro; IPR000189; SHprot_acsite.
InterPro; IPR000169; SHprot_acsite.
InterPro; IPR000185; VWF_A.
Pfam; PF00008; EGF; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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1258
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VQEPPTVEDLEPPYNTTFQERVANQRIEF-PCPAKGTPKPTIKWLHNGRELTGREPGISI 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESPPGS------SPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIIKNLKIEDSDTYICEVEDQ----KEEVQLLVFGLTA----NSDTHLLQGQSLTLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP
                                                                                                                                       TSPKLML----SLKLENKEAKVSKREKPVWV---LNPEAGMWQCLL----SDSGQVLLE
                                                                                                                                                                                     -ETRTSDSGMYLCVATNIAGNVTQAVKLNVHVPPKIQRGPKHLKVQVGQRVDIPCNAQGT
                                                                                                                                                                                                                                      LEAKT-----
                                                                                                                                                                                                                                                                                   RGLSQDKPVEISVLAGEEVTLPCEVKSLPPPIITWAKETQLISPFSPRHTFLPSGSMKIT
                                                                                                                                                                                                                                                                                                                            KRVTQDPKLQMGKKLPLHLTLP---QALP----
                                                                                                                                                                                                                                                                                                                                                                             S----SAKFSAGADGSLYVVSPEGEESGEYVCTATNTAGYAKRKVQLTVYVRPRVFGDL
                                                                                                                                                                                                                                                                                                                                                                                                                          SFPLAFTVEKLTGS-GELWWQAERASSSKSWI----TFDLKNKEV-----SV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NVAGTNNKTTSVVVHVLPTIQHGQQILSTIEGIPVTLPCKASGNPKPSVIWSKKGELIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLLAGNPIPERRWIKNSAMLLQNPYITVRS-----DGSLHIERVQLQDGGEYTCVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LFILNLWASDKGTYICEAENQFGKIQSETTVTVTGLVAPLIGISPSVANVIEGQQLTLPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSNVTLPCYVQGYPEPTIKWRRLDNMPIFSR--PFSVSSISQLRTGA-------
                                            ----SNIKVL-PTWSTPVEPKSCDKTHTCPPCPAP-----
                                                                                        PLPVITWSKGGSTMLVDGEHHVSNPDGTLSIDQATPSDAGIYTCVATNIAGTDETEITLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.6%; Scilarity 19.5%; Pr
Conservative 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Immunoglobulin domain.
AA; 613660 MW; F000B3
                                                                                                                                                                                                                                 -----GKLHQEVNLVVMRATQLQK------NLTCEVWGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -TVLQNQKKVEFKIDIVVLAFQKAS----SIVYKKEGEQVEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 0.00019;
7; Mismatches 253; Indels 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F000B319CED7B52C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 5636;
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                                              ELLG-GPSVFL
                                                                                                                                                                                                                                                                                                                               QYAGSGNLTLA
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                                              421
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                                                                                                             Query Match
Best Local S
Matches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q90524 PRELIMINARY; PRT; 268 AA.
Q90524;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-NOV-1996 (TrEMBLrel. 25, Last annotation update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
NOVEL antigen receptor (Fragment).
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
NOVEL TAKEND (Nurse shark).
G1nglymostoma cirratum (Nurse shark).
G1nglymostoma cirratum (Nurse shark).
Elasmobranchii; Galeomorphii; Galeoidea; Orectolobiformes;
G1nglymostomatidae; Ginglymostoma.
NCBI_TaxID=7801;
                                                                                                                                                                    Receptor.
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Greenberg A.S., Avila D., Hughes | Flajnik M.F.;
                                                                                                                                                                                                          Pfam; PF00047; ig; 2.
SMART; SM00407; IGc1; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                         EMBL; U18680; AAB48352.1; -. HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                    Greenberg A.S.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                       "A new antigen receptor gene family that undergoes rearrangement extensive somatic diversification in sharks."; Nature 374:168-173(1995).
                                                                                                                                                                                                                                                              InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                            GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-240 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91
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                                                       14
 66
                                                                                                                65,
                                                                                                                             Similarity
 TISKGGRYVETVNSGSKSFSLRIND----
                                                                                 PSVFLFPPKPKDTLMISRTPE------VTCVVVDVSHEDPEVKFNWYVDG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTCLVKGF-YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYKCKVSNKA-------LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVS 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNQLTNLFCEVEGTPSPIIMWYKDNVQVTESST----IQTVNNGKILKLFRATPED---A 1426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FPPKPKDTLMI--SRTP----EVTCVVVDVS-----HEDPEVK------
                                                                                                                                                                    268
268 AA;
                                                                                                             5.4%;
llarity 24.3%;
Conservative 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -EEGTLLVIASVTPYDNGEYICVAVNEAGTTERKYNLKVHVPPVIKDKEQVSNVSVL
                          VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV--SNKALPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1531
                                                                                                                                                                      268
29579 MW;
                                                     -TARVDQTPQEITKETGESLSINCVLRDSNCALPSTYWNRKKSGSTNEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG
                                                                                                              39;
                                                                                                           Score 186; DB 13;
Pred. No. 4.9e-06;
9; Mismatches 98
                                                                                                                                                                      OCDE524DD6E9FDC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M., Hughes A.,
----LTV-----EDSGTYRCKVYRKNWAYDCG
                                                                                                                                        DB 13;
                                                                                                              98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McKinney
                                                                                                                                       Length 268;
                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E.C.,
                                                                                                              66;
                                                                                                           Gaps
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Best Local
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Q8WU38;
Q1-MAR-2002 (TrEMBLrel. 20,
Q1-MAR-2002 (TrEMBLrel. 20,
Q1-MAR-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein. SEQUENCE 573 AA; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ EMBL; BC021276; AAH21276.1; -. PIR; S21205; S21205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2003 (TrEMBLre:
Hypothetical protein.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Tonei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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InterPro; IPR003596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity hes 151; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234
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RATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQ | | :: : :||
                                                                                                                                                                                                                                                                                                                                                                                                     ALYYCAKHGSGSYI-----GYYYGMD----VWGQGTTVTVSSAPTKAPDVFPIISGCRHPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSV-----QCRSPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QAPGKGLEWVSGISWNSGSIGYADSVKGRFTIS-RDNAKNSLYLQMV-----SLRAEDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MNRGVPFRHLLLVL---QLALLPAATQGNKVVLGKKGDTVELTCTAS--QKKSIQFHWKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSWQKNTKTITSGFATTSPVKTSSNDFSCASLLKVPLQEWSRGSVYSCQVSHSATSSNQR
                                                                                    IF--RWPESPKAQAS--
                                                                                                                                  VSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGS---GNLTLALEAKTGKLHQEVNLVVM
                                                                                                                                                                                      MGTQSQPQRTFPEIQRRDSYYMTSSQLSTPLQQWRQGEYKCVVQHTASKS-----KKE
                                                                                                                                                                                                                                          KKEGEQVEFSFP-----LAFTVEKLTGSGELWWQAE-----RASSSKSWITFDLKNKE
                                                                                                                                                                                                                                                                                                DNSPVVLACLITGYHPTSVTV----TW-----
                                                                                                                                                                                                                                                                                                                                               GKN-----IQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLAFQKASSIVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNQIK-----ILGNQGSF----LTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MELGLSWIFLLAILKGVQCEVQLVESGGGLV----QPGRSLRLSCAASGFTFDDYAMHWVR
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; Ig_MHC.
; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.4%; Score 184.5; DB 4;
21.0%; Pred. No. 1.9e-05;
tive 77; Mismatches 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                 -SVPTAQPQAEGSLAKATTAPATTRNTGRGGEE-
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                                                                                                                                                                                                                                                                                                                                                                                                        162
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Q908W47
IDD08W4
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InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; 19; 1.
SMART; SM00407; IG:; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 130 AA; 14253 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Pancreas;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                            EMBL; AK007622; BAB25142.1;
PIR; S22760; S22760.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9D8W4;
01-JUN-2001
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                                                                                                                                                                                                                                                                     MGD; MGI:1916426; 1810027001Rik.
                                                                                                                                                        InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig cl.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                  Nature 409:685-690(2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1810027001RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                             Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      810027001Rik protein.
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      438197975E766E54 CRC64;
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Q8N355
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Matches 50
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InterPro; TPR007110; Ig-1ike.
InterPro; IPR003597; Ig c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; BC028990; AAH28090.1;
PIR; S12441; S12441.
Interpro-
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SMART; SM00409; IG; 2.
SMART; SM00407; IGC1; 1.
SMART; SM00406; IGV; 1.
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Homo sapiens (Human).
Bukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8N355;
01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2003 (TrEMBLrel. 25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50835; IG_LIKE; 2. PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
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50; Conserv
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                                                                                                                                                                                                                                 GSFFLYSKLTVDKSRWQQGNVFSCSVMHE
                                                                                                                                                                                                                                                                                R-EPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOP-ENNYKTTPPVLDSD
                                                                                                                                                                                                                                                                                                                                                                             RPSGIPERFSGSNSGNTATLTISRVDAGDEADYYCQLWDSSSDHPVVFGGGTKLTVLGQP
                                                                                                                                                                                                                                                                                                                                                                                                                          KPR----EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI----EKTISKAKGQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSVTSYVLTQPPSVSVAPGQTARITCGGNNIGSK----SVHWYQQKPGQAPVLVVYDDSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY-----VDGVEVHNAKT
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234 AA; 2
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larity 23.9%;
Conservative 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 183; DB 4;
Pred. No. 6.8e-06;
2; Mismatches 99
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Pred. No. 2.7e-06;
8; Mismatches 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC848CAEBA4A9D63 CRC64;
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Best Local S
Matches 112
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EMBL; U32086; AAA84866.1; --
HSSP; P19320; 1VCA.
GO; GO; 0016022; C:membrane; IEA.
GO; GO:0016337; P:cell-cell adhesion; IE
InterPro; IPR003987; ICAM VCAM-1.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003598; VGAM-1.
Pfam; PF00047; ig; 7.
PRINTS; PR01472; ICAMVCAM1.
SMART; SM00408; IGc2; 4.
PROSITE; PS50835; IG_LIKE; 5.
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Ballantyne C.M., Clubb F.J., Perrard J.L., Radovencovic B.,

Youker K.A., Smith C.W., Entman M.L., Hawkins H.K., Frazier O.H.,

Willerson J.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Vascular cell adhesion molecule-1. Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin domain.
SEQUENCE 739 AA; 81412 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arteriopathy in the Dog.";
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases
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[1]
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Increased Expression of VCAM-1 and ICAM-1 in Early Cardiac Allograft
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Local 5.
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644 TVLKSRDGAY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 5.3%; Score 182.5; DB 6
Similarity 21.5%; Pred. No. 3.8e-05;
12; Conservative 96; Mismatches 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTLTLESPPGSSPS----VQCRSPRG--KNIQGGK-TLSVSQLELQDSGTWTCTVLQNQK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGNATITLIAMRLEDSGTYVCEGVNEVGKDGKEVELIVQEKPFTVEISPGPQIIAQIGDS 330
                                                                                                                                                                                                                               LSEDPILTLTSAKMEDSGIYVCEGINQAG--ISRKEVELI----IQVAPKDI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSKSWI-----TFDLKNKEVSVKRVTQDPKLQMGKKL----PLHLTLPQALPQYAGSGN
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                                                                                                                                                                   CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV--DGVEVHN 465
                                                                                                                                                                                                                                                                                                                                                                             LTLALEAKTGKLHQEVNLVVMRATQLQK----NLTCEVMGPTSPKLMLSLKLENKEAKVS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESKSFLEDMDKKSLETKSLEMTFIPTTED----TGKVLVCLAKLHIDEMEFEPKQRQS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KVEFKIDIVVLAFQK-----ASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERAS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VVLTCGVTDCESPSFSWRTQIDSPLSGTVKVEGAKSTLTLSPVNLENEHSYLCTVTCGHK
                                                                                                                                                                                                                                                                                        KREKPVWVLN----PEAGMWQCL-LSDSGQVLLESNIKVLPTWSTPVEPKSCDKTHTCPP
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                                                      AKTKPREEQYNSTYRVVSVLTVLHQDWL-NGKEYKCKVSNKA
                                                                                                                                                                                                                                                                                                                                                  -TOTLYVNVAP--RDTTVVVSPSSIVEEGSPVNMTCSSDGLPAPNILWSRRLSNGRLQ-S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLEKGIKVDLYSFPRDPEVEMSGLLVDGNPVTVSCEVPNVYPSDRL--EIEL-FKGETII 447
                                                                                                            -QLIAFPSESV---KEGDTVIIS--
----TIHKVQLEDAGVYECESKNEA 674
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                                                                                                               --CTC-----GNVPKTWIILKKKAETGD
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RESULT 96 Q63669

dg dg	Qy db	Db Qy	Db Qy	Db Qy	dd Vy	QY dd	Db Qy	Query Best Match	CHERON REPORT OF THE CONTROL OF THE	
435 TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHODWLN 49:	6 GQVLLESNIKVLPTWSTPVEPKSCDKTHTCPPCPAPELLGGPSVELFP-PKPKOTLMISR 4	MLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDS 3	256 LKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALBAKTGKLHQEVNLV 319 : : :	196 KIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELMWQAERASSSKSWITFD 25: 	143 LESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEF 199	93 PLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLT 143	33 KGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNF 92	ry Match 5.3%; Score 182.5; DB 11; Length 739; t Local Similarity 20.8%; Pred. No. 3.8e-05; ches 124; Conservative 87; Mismatches 195; Indels 191; Gaps 28	01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 02, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Vascular cell adhesion molecule 1 precursor. VCAM-1. RATTUS norvegicus (Rat). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. MCBI TaxID=10116; [1] TaxID=10116; STRAIN-Sprague Dawley; TISSUE=Lung; STRAIN-Sprague Dawley; TISSUE=Lung; STRAIN-Sprague Dawley; TISSUE=Lung; MEDLINE=2305064; PubMed=1377031; Williams A.J., Atkins R.C., Fries J.W., Gimbrone M.A.Jr., Cybulsky M.I., Collins T.; "Nucleotide sequence of rat vascular cell adhesion molecule-1 cDNA."; Biochim. Biophys. Acta 1131:214-216(1992). EMBL; X63722; CAA45254.1; EMBL; X63722; CAA45254.1; HSSP; P19320; IVCA. GO; GO:0016337; P:cell-cell adhesion; IEA. GO; GO:0016337; P:cell-cell adhesion; IEA. GO; GO:001637; P:cell-cell adhesion; IEA. GO; GO:001637; P:cell-cell adhesion; IEA. InterPro; IPR003398; VCAM-1. InterPro; IPR003398; VCAM-1. Pfam; PF00047; 1g; 5. InterPro; IPR003398; VCAM-1. PRINTS; PR01474; VCAM1. SNART; SM00408; IGC2; 4. PROSITE; PS09835; IG LIKE; 5. Immunoglobulin domain; Signal. SIGNAL 1 24 POTENTIAL. DASCULE 1.	63669 PRELIMINARY; PRT; 739 AA.

16448

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16497

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RESULT

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Best Local S
Matches 128
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-i- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
EMBL; AB055861; BAB64297.1; -.
GO: GO:005975; P: Carbohydrate metabolism; IE InterPro; IPR000577; FGGY kin.
InterPro; IPR000577; FGGY kin.
InterPro; IPR003961; FN_III-
InterPro; IPR003961; FN_III-
InterPro; IPR003598; Ig_12.
InterPro; IPR003598; Ig_12.
InterPro; IPR003598; Ig_22.
InterPro; IPR003598; Ig_23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00041; fn3; 5.
Pfam; PF00047; ig; 49.
Pfam; PF00018; SH3; 1.
SMART; SM00408; IGc2; 13.
SMART; SM00326; SH3; 1.
SMART; SM00326; SH3; 1.
PROSITE; PS0093; PGGY_KINASES_1; 3
PROSITE; PS0002; SH3; 1.
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Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacid
Astacoidea; Cambaridae; Procambarus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mmunoglobulin domain; SH3 domain.
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                                                                                 16402
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                             247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
SSKSWITEDLKNKEVSVKRVTQDFKLQ-----MGKKLFLHLTLFQALFQYAGSGNLTL
                                                                                                                                                                                   ITWYKDEVEIRFSDHYQLSIDGK----VQRLMVYNCQFEDSGTYRAVVGKSECSATLKVE
                                                                                                                                                                                                                                                                                           MEATLSDEGEYTCVLGDQECTAELTVRELPAEIVRKMKDQVVSKGDRATMEVELTKGDAV
                                                                                                                                                                                                                                                                                                                                                                                          VEVT---NEKATVTWH-KDGEEITEHHERFKLVSQGKTR-----KLVL
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                                                                                                                                                                                                                                                                                                                                         KNLKIEDSDTYICEVEDQKEEVQLLVFGLTAN----SDTHLLQGQSLTLTLESPPGSS-
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                                                                                                                                                                                                                                    -----PSVQCR-----SPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKID
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l (TrEMBLrel.
3 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17352 AA; 1962348 MW;
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19.9%;
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19,
25,
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                                                                               EGDFSKKLPAQMDVNFKTDATFVVE-ITKDYEVKWLREGAELSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 182; DB
Pred. No. 0.00
03; Mismatches
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Last sequence update)
Last annotation updat
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                                                                                                                                -QVEFSFPLAFTVEKLTGSGELWW----QAERAS
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NFTAT-----
                                                                                                                                                               AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
                                     NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
                                                                       YVKVCEPVRAEPPVVKEQLQAVVTGLHQEVVLRCVVTATPTPKIDWLKDGKPVSGNTSYE
                                                                                                       QVYTLPPSRDELTKNQVSLTCLVKGFYPSDI-----AVEWESNGQPEN---
                                                                                                                                                                                                                                                                                TISEQEASITIKQVENIDCGEYRLKLCNDCGAAYADFTLKILDKPSQPGTPEPMEVTNV- 16608
                                                                                                                                                                                                                                                                                                                  KVSKREKPV---WVLNPEAGMWQC-LLSDSGQVLLESNIKVLPTWSTPVEPKSCDKTHTC
                                                                                                                                                                                                                                                                                                                                                                                    ALEAKTGKLHQEVNLVVMRATQLQKNLTCEV--WGPTSPKLM-----LSLKLENKE---A
                                                                                                                                           -----KITQSTTVVTSLTT-HE-----EYCFRVS-----AENEIGRSEASNASR
                                                                                                                                                                                                                                              PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
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     LTIKETMETSGGMYTCRASNEA
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RESULT 98
Q8ISF3
       ProDom; PD000001; Prot_kinase; 1
SWART; SW00406; FN3; 1.
SWART; SW00408; IGC2; 19.
SWART; SW00200; S_TKC; 1.
SWART; SW00210; TyrKC; 1.
SWART; SW00219; TyrKC; 1.
PROSITE; PS00107; PROTEIN_KINASE
PROSITE; PS001108; PROTEIN_KINASE
PROSITE; PS00108; PROTEIN_KINASE
                                                                                                                                                                                InterPro; IPR003961; FN III.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig _c2.
InterPro; IPR000719; Prot kinase.
InterPro; IPR008270; Ser thr pkinase.
InterPro; IPR008271; Ser thr pkin AS.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                EMBL; AY130758; AAN61521.1; -. GO: GO:005524; F:ATP binding; IEA. GO:0005524; F:ATP binding; IEA. GO:0004674; F:protein serine/threonine kinase activity; IEA. GO:0004674; F:protein-tyrosine kinase activity; IEA. GO:0004713; F:protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OBISF3, PRELIMINARY;
OBISF3;
O1-MAR-2003 (TrEMBLrel. 23,
O1-MAR-2003 (TrEMBLrel. 23,
O1-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                              Flaherty u., occ....
Borodovsky M., Benian G.;
"Titins in Caenorhabditis elegans with Unusual Features:
"Titins in Caenorhabdition of Kinase Activity and Two New
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=22269627; PubMed=12381307;
MEDLINE=7 Gernart K., Shmeleva N.,
                                                                                                                                                                                                                                                                                                                                                             Elastic Regions.
J. Mol. Biol. 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                      Pfam; PF00041; fn3; 2.
Pfam; PF00047; ig; 19.
Pfam; PF00069; pkinase; 1
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; IG LIKE; 18.
; PRŌTEIN KINASE ATP; 1
; PROTEIN KINASE DOM;
; PROTEIN KINASE ST; 1
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QBISF4;
QBISF4;
01-MAR-2003 (TrEMBLrel. 2
01-MAR-2003 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2
SEQUENCE FROM N.A.
MEDLINE=22269627; PubMed=12381307;
Flaherty D., Gernert K., Shmeleva |
Borodovsky M., Benian G.;
                                                                                                                            Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                            301KDa_1 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VGLEDEGTYTITAENEKGKIRQNTEVSV---TKSKEVKEKKKEKKKVEKKDEGKKXPGRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREK-----PVWVLN----PEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDNTATLVIENVTDELCGTYTAVANNQFGDVHTSAQLTISGSEAKKIAASLPYFIIELKP
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                              Shmeleva N.,
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SMART; SM00060; FN3; 1.

SMART; SM00108; IGC2; 19.

R SMART; SM00210; TyrKC; 1.

R PROSITE; PS500315; IG LIKE; 18.

R PROSITE; PS500107; PROTEIN KINASE DOM; 1.

R PROSITE; PS500108; PROTEIN KINASE TOM; 1.

R PROSITE; PS500108; PROTEIN KINASE ST; 1.

R PROSITE; PS00108; PROTEIN KINASE ST; 1.

C SEQUENCE 2708 AA; 300729 MW; 2BBEEBE856FA4571 CRC
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Best Local :
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InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig_c2.
InterPro; IPR000719; Prot kinase.
InterPro; IPR000719; Ser_thr_pkinase.
InterPro; IPR0008271; Ser_thr_pkin AS.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Titins in Caenorhabditis elegans with Unusual Features: Domains, Novel Regulation of Kinase Activity and Two New Elastic Regions.";
J. Mol. Biol. 323:533-549(2002).

EMBL; AY130758; AAN61520.1; -.
GO; GO:000524; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0004713; F:protein amino acid phosphorylation; IEA.
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Pfam; PF00047; ig; 19.
Pfam; PF00069; pkinase; 1.
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137; Conserv
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        DKKSNHKLV-CHAVQSQD--TGK-YRCVVTNKYGYAESECNVAV----
                                               QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
                                                                                          QAGQQIML-----
                                                                                                                                   LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                          GTFNCLIENELGQASASCQVTIFN-----KPASLQSTPDHSLERNLVPTLQKALNNESA
                                                                                                                                                                                                                  GMWQCLL-SDSGQVLLESNIKVLPTWSTPVEPKSCDKT--HTCPPCPAPEL------
                                                                                                                                                                                                                                                           NRDDEFE--IAVEFSGTFTP----SVKWYKENLQIVPDEKIDVATTSTSSILNLKSQEEN
                                                                                                                                                                                                                                                                                                MRATQLOKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREK-----PVWVLN----PEA
                                                                                                                                                                                                                                                                                                                                           EYIFRVAGKNKQGLGEWSEMTSTLKTASVGQAPQF----TISPQSK-----IIA
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                                                                                          -TCRISSRSESTVA------
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Pred. No. 0.
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      Pfam; PF00041; fn3; 2. Pfam; PF00047; ig; 19.
Pfam; PF00067; pkinase; 1.
PRINTS; PF00061; PKTYPEIII.
PRODOM; PF000001; PROTEXINASE; 1.
SMART; SM00060; FN3; 2.
SMART; SM00200; S. TKC; 1.
SMART; SM00220; S. TKC; 1.
SMART; SM00220; S. TKC; 1.
SMART; SM00210; TYFKC; 1.
PROSITE; PS00107; PROTEIN KINASE DOM; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
HYDOTHETICAL PROTEIN KINASE ST; 1.
HYDOTHETICAL PROTEIN KINASE ST; 1.
                                                                                                                                                                                        InterPro; IPR003962; FNIII subd.
InterPro; IPR003961; FN III.
InterPro; IPR008957; FN III-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR007598; Ig-2.
InterPro; IPR007290; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                             Waterston R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; U8002; AAM29672.1; -.
EMBL; U8002; AAM29672.1; -.
WormPep; F12F3.2a; CE30755.
G0; G0:0005524; F:ATP binding; IEA.
G0; G0:0004674; F:protein serine/threonine kinase activity
G0; G0:0004674; F:protein-tyrosine kinase activity; IEA.
G0; G0:0004713; F:protein-tyrosine kinase activity; IEA.
G0; G0:0016740; F:transferase activity; IEA.
G0; G0:0006468; F:protein amino acid phosphorylation; IEA.
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[2]
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Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fulton B., Wohldmann P., "The sequence of C. elegans Submitted (JAN-1997) to the
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STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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01-OCT-2003
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rinae; Caenorhabditis.
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EMBL/GenBank/DDBJ
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                                                                                                            QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
                                                                                                                                                                                                                  GMWQCLL-SDSGQVLLESNIKVLPTWSTPVEPKSCDKT--HTCPPCPAPEL------
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CKLSISKAESDDMGVYVCS
                      SKLTVDKSRWQQGNVFSCS
                                                 FSATLSDSTAILGHNITLECKVEGSPAPE
                                                                                                   DKKSNHKLV-CHAVQSQD--TGK-YRCVVTNKYGYAESECNVAV-
                                                                                                                                                   QAGQQIML
                                                                                                                                                                                                   GTFNCLIENELGOASASCOVTIFN-----KPASLOSTPDHSLERNLVPTLOKALNNESA
                                                                                                                                                                                                                                                      NRDDEFE -- IAVEFSGTPTP----
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                                                                         -----RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
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nilarity 20.2%;
Conservative 99
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Pred. No. 0.00036;
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                                                 -VSWTKDGERISTTRRIRQTQDENGN----
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N-PSDB; AAN90357.
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diagnosis; CD4;
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02-NOV-1992
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein may comprise the complete CD4 sequence, the 370 AA extracellular region and the membrane spanning domain, or the extracellular region. The Ig heavy chain is pref. from IgM, IgG1 or IgG3. The following are specifically claimed: fusion proteins CD4H-gamma-1, CD4Mmu, CD4E-gamma1, and CD4Mmu (No.67608), pCD4P-gamma (No.67609) and pCD4E-gamma-1 (No.67609). The plasmid containing (pCD4E-gamma-1) has been deposited in E. coli (MC1061/P3) at the ATCC under accession number 67610. (Updated or 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                           LVFGLTANSDTHLLQGQSLTLTLESSPGSSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                631 AA;
                                                                    ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
                                                                                                        NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
                                                                                                                       NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
                                                                                                                                                                                                                                LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPV-----EPKSCDKTHTCPPCPAPELLG
                                                                                                                                                                                                                                                                                   LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                                                                                                                                                                                         QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
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                   WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEEPKSCDKTHTCPPCPAPELLG
                                                                                                                                                                                                                                                                    LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                    ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
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Pred. No. 1.8
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llular region. The
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AAB19508 standard; protein; 631 B

AAB19508

09-JAN-2001 (first entry)

CD4-IgG1 fusion protein CH4Egammal

RESULT 2
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AC AAB1
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CD4XX
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GD13
XX CD4; IgG1; human; CD4Egamma1; fusion gp120; therapy; diagnosis. protein; immunoglobulin; HIV;

The fusion protein genes of the invention pref, comprise cDNA sequences which encode CD4 or a fragment which binds gp120 ligated to an expressic plasmid which encodes an antibody in which the variable region of the gene has been deleted (see WO87-02671). The CD4 portion of the fusion

n expression of the fusion

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Query Match
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Matches 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of fusion protein CD4Egammal comprising the extracellular portion of CD4, which binds to HIV gpl20, linked at its C-terminus to the human IgG1 heavy chain. To obtain the fusion protein, DNA encoding CD4 was linked to IgG1 DNA at the Esp site upstream of the hinge region (see AAA50661). Fusion protein CD4Egammal and a nucleic acid encoding it are claimed. Also claimed are a vector comprising the nucleic acid, and a method of producing the fusion protein in secreted form using a transformed host cell. The fusion protein may further comprise a therapeutic agent, radiolabel or NMR imaging agent. The fusion protein can be administered to an animal (including humans) for treatment of HIV or SIV infection, and can also be used in assays for HIV or SIV, imaging and tissue stains. IgG1 fusion proteins such as CD4Egammal provide both complement-mediated and cell-mediated immunity
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09-JUN-1992;
12-APR-1993;
04-FEB-1994;
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                                                                                                                                                                                                                                LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                              QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                                                                                                                              TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                                                                                                                                                                                                                      ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                      TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                                                                                                                                      LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                    QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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89US-00299596.
92US-00896781.
93US-00057952.
94US-00191708.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 3268.5; DB 3; Length 631;
Pred. No. 1.8e-170;
0; Mismatches 1; Indels 5;
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                                                                 This invention describes a novel nucleic acid (I) encoding a fusion protein comprising a DNA sequence encoding amino acids 1-173 of CD4 (II) and a DNA sequence encoding a human immunoglobulin (Ig) heavy or light chain (III). The products pf the invention have anti-human immunodeficiency virus (HIV) activity and are capable of binding to gpl20. The fusion protein is useful for treating human immunodeficiency virus (HIV) or similar immunodeficiency virus (SIV). This sequence represents the fusion protein CD4Egammal which is constructed from CD4
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23-JAN-1989;
09-JUN-1992;
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                                                                                                                                                                                                                                                                                                                                                                    Fusion protein useful for the treatment
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                                                                                                                                                                                                                                                                                                                   Example 1;
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                                                   linked to human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tein; human; CD4; IgG1; immunoglobulin;
immunodeficiency virus; CD4Egamma1.
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89US-00299596.
92US-00896781.
93US-00057952.
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                                                   IgG1 upstream of the hinge region
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Best Local Simi
Matches 624;
                      20-JAN-1989;
                                                                   CA1340741-C.
                                                                                                                             secreted
                                                                                                                                                               CD4-Ig
                                                                                                                                                                                      14-MAR-2000
                                                                                                                                                                                                                                   AAY59169
  20-JAN-1989;
                                               14-SEP-1999
                                                                                                                             extracellular; CD4; gp120; immunoglobulin;
eted protein; SIV infection; medicament.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                            WOOGNVFSCSVMHEALHNHYTOKSLSLSPG
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                                                                                                                                                               protein CD4Egammal.
 89CA-00588749
                        89CA-00588749
                                                                                                                                                                                                                                  protein;
                                                                                                                                                                                      entry)
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99.0%;
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Pred. No. 1.8e-170;
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The invention provides a fusion gene encoding a fusion protein that comprises an extracellular CD4 DNA sequence or its fragment which binds to HIV gp120 when fused to an immunoglobulin (1g) chain and the DNA sequence of an Ig heavy or light chain, where the DNA sequence which encodes the variable region has been replaced with the DNA sequence which encodes extracellular CD4 or its gp120 binding fragment. The fusion protein is capable of being secreted. The fusion proteins are useful for treating HIV or SIV infections in animals, preferably humans. They are also useful for producing medicaments which can be used for treating HIV or SIV infections. The present sequence represents the fusion protein in in humans. The present sequence represents the fusion protein CD4Egammal where the CD4 is linked to human IgG1 at the Esp site upstream
Sequence
                                                                                                                                                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-063015/06
N-PSDB; AAZ48202.
                                                                                                                                                                                                                                                                                                                          Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GEHO)
                                                                                                                                                                                                                                                                                                                                                                     fusion gene encoding immunoglobulin-CD4 fusion proteins, useful treatment of HIV or simian immunodeficiency virus infections.
                                      hinge region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GEN
631 AA;
                                                                                                                                                                                                                                                                                                                          Page 37-46; 89pp; English
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Ś S Ş δ 8 뭐 밁 밁 Ş 밁 S В S 밁 5 밁 Ş 밁 S B S Matches 624; Query Match Best Local 541 481 421 416 361 361 301 301 241 241 181 181 121 121 61 61 μ Similarity LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPV-----EPKSCDKTHTCPPCPAPELLG LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD GPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKFREEQY LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK WQQGNVFSCSVMHEALHNHYTQKSLSLSPG NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEEPKSCDKTHTCPPCPAPELLG LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA Conservative 95.7**%**; 99.0**%**; Score 3268.5; DB 3 Pred. No. 1.8e-170; 0; Mismatches 1; 625 ω --Indels Length 631; 5 475 420 360 300 240 240 180 180 120 120 60 540 480

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RESULT 5
AAP93008
ID AAP9
XX AAP9
XX AAP9
XX AAP9
XX Gene
DE Gene
DE Gite
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DE Gite
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Best Local Similarity 85.'
Matches 624; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The fusion protein genes of the invention pref. comprise cDNA sequences which encode CD4 or a fragment which binds gpl20 ligated to an expression plasmid which encodes an antibody in which the variable region of the gene has been deleted (see WO87-02671). The CD4 portion of the fusion protein may comprise the complete CD4 sequence, the 370 AA extracellular region and the membrane spanning domain, or the extracellular region. The Ig heavy chain is pref. from IgM, IgG1 or IgG3. The following are specifically claimed: fusion proteins CD4H-gamma-1, CD4Mmu, CD4E-gamma1, and CD4Mmu (No.67608), pCD4P-gamma (No.67609) and pCD4E-gamma-1 (No.67609) at the ATCC under accession number 67611. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 729 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusion protein; immunoglobulin-like molecule; HIV; SIV; therapy; diagnosis; CD4; gp120; binding fragment; glycoprotein; variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetic construct which encodes site upstream of the CH1 region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin-CD4 fusion proteins - used for treating infections or detecting HIV or SIV in sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP325262-A.
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02-NOV-1992
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                                                                                LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                       ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                    MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Table 1,
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TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                                                                                                                                                                                                  MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                  LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                           ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89EP-00100913
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                                                                                                                                                                                                                                                                                                                                                                       Score 3219.5; DB Pred. No. 1e-167; O; Mismatches
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                                              22-JAN-1988;
23-JAN-1989;
09-JUN-1992;
12-APR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD4; IgG1; human; gp120; therapy; di
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                     88US-00147351.
89US-00299596.
92US-00896781.
93US-00057952.
94US-00191708.
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                                                                                                                                                                                                                                                                                                             note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD4Hgamma1; fusion protein; immunoglobulin;
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                                                                                                                                                                                                                                                                                                          "IgG1 heavy chain"
                                                                                                                                                                                                                                                                                                                                                      "CD4 extracellular
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Best Local Simi
Matches 624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of fusion protein CD4Hgammal comprising the extracellular portion of CD4, which binds to HIV gp120, linked at its C-terminus to the human IgG1 heavy chain. To obtain the fusion protein, DNA encoding CD4 was linked to IgG1 DNA at the Hind3 site upstream of the CH1 region (see AAA50660). Fusion protein CD4Hgammal and a nucleic acid encoding it are claimed. Also claimed are a vector comprising the nucleic acid, and a method of producing the fusion protein in secreted form using a transformed host cell. The fusion protein may further comprise a therapeutic agent, radiolabel or NMR imaging agent. The fusion protein can be administered to an animal (including humans) for treatment of HIV or SIV infection, and can also be used in assays for HIV or SIV, imaging and tissue stains. IgG1 fusion proteins such as CD4Hgammal provide both complement-mediated and cell-mediated immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 729 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD4-immunoglobulin fusion
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DB; AAA50660.
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                                                                                                                                                                                                                                   LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTP-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MNRGVPFRHLLLVLQLALLPAATOGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                   VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
                                                                                                                                                                                                                                                                               LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
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                                                                                                                                                                                                                                                                                                                                          QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
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                                                                                                                                                                                                                                                                                                                                                                                                                          TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
 YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA
                              VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
                                                                                           ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE
                                                                                                                                                      TAALGCLVVSYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY
                                                                                                                                                                                                                  LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEASTKGPSVFPLAPSSKSTSGG
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85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteins, useful for targeting gp120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 3219.5; DB Pred. No. 1e-167; O; Mismatches
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61

ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL

120

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MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK

Matches

624;

Conservative

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Mismatches

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103;

Gaps

Similarity

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   Query Match
Best Local
                                                                                                                                          The invention provides a fusion gene encoding a fusion protein that comprises an extracellular CD4 DNA sequence or its fragment which binds to HIV gp120 when fused to an immunoglobulin (Ig) chain and the DNA sequence of an Ig heavy or light chain, where the DNA sequence encoding the variable region has been replaced with the DNA sequence which encodes extracellular CD4 or its gp120 binding fragment. The fusion protein is capable of being secreted. The fusion proteins are useful for treating HIV or SIV infections in animals, preferably humans. They are also useful ifor producing medicaments which can be used for treating HIV or SIV infections in humans. The present the fusion protein CD4Hgammal where the CD4 is linked to human IgG1 at the Hind3 site
                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New fusion gene encoding immunoglobulin-CD4 fusion proteins, useful the treatment of HIV or simian immunodeficiency virus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIV; extracellular; CD4; gp120; immunoglobulin; Ig; secreted protein; SIV infection; medicament.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 25-36; 89pp; English.
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                                                                                             729 AA;
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